Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	559	methionine adj aminopeptidase$	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:01
L2	8602	(methionine or met) same muta$10	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02
L3	223	1 same 2	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02
L4	2380	methionine same cysteine same muta$10	US-PGPUB; USPAT	OR	OFF	2005/03/24 15:59
L5	121	4 same stab$8	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:00
L6	21573	oxidat$ near4 stab$8	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:27
L7	78	4 and 6	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:27
L8	2775	sulfur adj free	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:35
L9	1	8 near2 (protein$1 or enzyme$1)	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:36

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	559	methionine adj aminopeptidase$	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:01
L2	8602	(methionine or met) same muta$10	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02
L3	223	1 same 2	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02

PGPUB-DOCUMENT-NUMBER: 20050059803

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050059803 A1

TITLE: Immunosuppressant target proteins

PUBLICATION-DATE: March 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Berlin, Vivian	Arlington	MA	US	
Chiu, Maria Isabel	Boston	MA	US	
Cottarel, Guillaume	West Roxbury	MA	US	
Damagnez, Veronique	Cambridge	MA	US	

APPL-NO: 10/ 877320

DATE FILED: June 24, 2004

RELATED-US-APPL-DATA:

child 10877320 A1 20040624

parent continuation-of 09517491 20000302 US PENDING

child 09517491 20000302 US

parent continuation-of 08360144 19941220 US GRANTED

parent-patent 6150137 US

child 08360144 19941220 US

parent continuation-in-part-of 08250795 19940527 US PENDING

US-CL-CURRENT: 530/350

ABSTRACT:

The present invention relates to the discovery of novel proteins of mammalian origin which are immediate downstream targets for FKBP/rapamycin complexes.

RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. Ser. No. 08/250,795, filed May 27, 1994 and entitled "Immunosuppressant Target Proteins", the specification of which are incorporated by reference herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (68):

[0113] When expression of a portion of one of the subject RAP-binding proteins is desired, i.e. a trunction mutant, such as the RAPT1 polypeptides of SEQ ID Nos.2, 12 or 14, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It

is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing RAP-BP-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20050059010

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050059010 A1

TITLE: Macular degeneration diagnostics and therapeutics

PUBLICATION-DATE: March 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Stone, Edwin M.	Iowa City	IA	US	
Sheffield, Val C.	Coralville	IA	US	

APPL-NO: 10/ 619761

DATE FILED: July 14, 2003

RELATED-US-APPL-DATA:

child 10619761 A1 20030714

parent continuation-of 09322357 19990528 US GRANTED

parent-patent 6593104 US

child 09322357 19990528 US

parent continuation-in-part-of 09248757 19990212 US GRANTED

parent-patent 6417342 US

US-CL-CURRENT: 435/6, 435/21

ABSTRACT:

Therapeutics and diagnostics based on the identification of genetic mutations, which cause Macular Degeneration (MD) are disclosed.

---------- KWIC --------

Detail Description Paragraph - DETX (93):

[0126] When it is desirable to express only a portion of an EFEMP1. protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing MFGF derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20050059803

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050059803 A1

TITLE: Immunosuppressant target proteins

PUBLICATION-DATE: March 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Berlin, Vivian	Arlington	MA	US	
Chiu, Maria Isabel	Boston	MA	US	
Cottarel, Guillaume	West Roxbury	MA	US	
Damagnez, Veronique	Cambridge	MA	US	

APPL-NO: 10/ 877320

DATE FILED: June 24, 2004

RELATED-US-APPL-DATA:

child 10877320 A1 20040624

parent continuation-of 09517491 20000302 US PENDING

child 09517491 20000302 US

parent continuation-of 08360144 19941220 US GRANTED

parent-patent 6150137 US

child 08360144 19941220 US

parent continuation-in-part-of 08250795 19940527 US PENDING

US-CL-CURRENT: 530/350

ABSTRACT:

The present invention relates to the discovery of novel proteins of mammalian origin which are immediate downstream targets for FKBP/rapamycin complexes.

RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. Ser. No. 08/250,795, filed May 27, 1994 and entitled "Immunosuppressant Target Proteins", the specification of which are incorporated by reference herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (68):

[0113] When expression of a portion of one of the subject RAP-binding proteins is desired, i.e. a trunction mutant, such as the RAPT1 polypeptides of SEQ ID Nos.2, 12 or 14, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It

is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing RAP-BP-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20050059010

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050059010 A1

TITLE: Macular degeneration diagnostics and therapeutics

PUBLICATION-DATE: March 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Stone, Edwin M.	Iowa City	IA	US	
Sheffield, Val C.	Coralville	IA	US	

APPL-NO: 10/ 619761

DATE FILED: July 14, 2003

RELATED-US-APPL-DATA:

child 10619761 A1 20030714

parent continuation-of 09322357 19990528 US GRANTED

parent-patent 6593104 US

child 09322357 19990528 US

parent continuation-in-part-of 09248757 19990212 US GRANTED

parent-patent 6417342 US

US-CL-CURRENT: 435/6, 435/21

ABSTRACT:

Therapeutics and diagnostics based on the identification of genetic mutations, which cause Macular Degeneration (MD) are disclosed.

---------- KWIC ---------

Detail Description Paragraph - DETX (93):

[0126] When it is desirable to express only a portion of an EFEMP1. protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing MFGF derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20050032221

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050032221 A1

TITLE: Dominant negative variants of methionine aminopeptidase 2 (MetAP2) and clinical uses thereof

PUBLICATION-DATE: February 10, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Chang, Yie-Hwa	St. Louis	MO	US	
Micka, William S.	St. Louis	MO	US	
Vetro, Joseph A.	Lawrence	KS	US	

APPL-NO: 10/ 712359

DATE FILED: November 13, 2003

RELATED-US-APPL-DATA:

child 10712359 A1 20031113

parent continuation-of 09943123 20010830 US PENDING

US-CL-CURRENT: 435/456, 424/93.2

ABSTRACT:

Inhibitors of type 2 methionine aminopeptidases ("MetAP2"), specifically dominant negative variants of MetAP2, both polypeptides and encoding polynucleotides, are provided. Also provided are methods of treating subjects suffering from cancer, diseases mediated by the immune system or opportunistic infections using inhibitors of MetAP2. Also provided are high through put screens and assays to detect and identify inhibitors of MetAP2 and downstream effectors of MetAP2.

---------- KWIC ---------

Detail Description Paragraph - DETX (17):

[0047] Methionine aminopeptidase type 2 (MetAP2, EC 3.4.11.18) cotranslationally removes N-terminal methionine from nascent polypeptides when the second residue is small and uncharged. MetAP2 consists of two domains: a conserved C-terminal catalytic domain, i.e., the "aminopeptidase domain", and an N-terminal polylysine domain predicted to mediate ribosome or eIF2 association, i.e., the "translation domain". According to the present invention, a dominant negative mutant of MetAP2 has been generated which is catalytically inactive against a peptide substrate. In a preferred embodiment, the conserved histidine of the catalytic domain [histidine 231 ("His.sup.231") of human (SEQ ID NO:12), mouse (SEQ ID NO:13) or rat (SEQ ID NO:17) MetAP2, or histidine 174 ("His.sup.174") of yeast MetAP2 (SEQ ID NO:14)] is replaced with another amino acid, preferably a non-conserved amino acid, more preferably an alanine. It is demonstrated herein that overexpression of a variant yeast MetAP2 dominant negative variant (H174A) in a yeast map1 null strain, which does not express a functional MetAP1 polypeptide, under the strong constitutive

GPD promoter was lethal whereas overexpression under the weaker regulatable GAL1 promoter significantly inhibited growth (Example 1). These observations suggest that the H174A mutant interferes with wild-type MetAP2 function in a dose-dependent manner. It is herein demonstrated that variant forms of human MetAP2, which lack aminopeptidase function, also have dominant negative activity. Specifically, a variant human MetAP2 comprising a H231A mutation was administered to human vascular endothelial cells in culture and was shown to inhibit vascular endothelial cell growth and endogenous aminopeptidase activity (Example 3). Thus, given that both yeast H171A MetAP2 and human H231A MetAP2 exhibit dominant negative activity, the invention encompasses any and all polypeptides comprising any variant MetAP2 polypeptides that possess dominant negative activity.

PGPUB-DOCUMENT-NUMBER: 20050019801

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050019801 A1

TITLE: Stem cell-based methods for identifying and characterizing agents

PUBLICATION-DATE: January 27, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Rubin, Lee L.	Wellesley	MA	US	
Kotkow, Karen	Jamaica Plain	MA	US	
Lai, Cheng-Jung	Belmont	MA	US	

APPL-NO: 10/ 861040

DATE FILED: June 4, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60476011 20030604 US

US-CL-CURRENT: 435/6, 435/366 , 435/7.2

ABSTRACT:

The present invention provides methods of identifying and/or characterizing agents that promote differentiation of stem cells to a particular differentiated cell type. The invention further provides methods of treating injuries and degenerative diseases by administering agents that promote the differentiation of stem cells to particular differentiated cell types.

RELATED APPLICATIONS

[0001] This application claims priority to U.S. provisional application 60/476,011, filed Jun. 4, 2003, the disclosure of which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (133):

[0210] When it is desirable to express only a portion of a protein, such as a form lacking a portion of the N-terminus, e.g. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the enzyme methionine aminopeptidase (MAP).

PGPUB-DOCUMENT-NUMBER: 20050004028

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050004028 A1

TITLE: Vertebrate embryonic pattern-inducing proteins and uses related thereto

PUBLICATION-DATE: January 6, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ingham, Philip W.	Oxford	MA	GB	
McMahon, Andrew P.	Lexington	MA	US	
Tabin, Clifford J.	Cambridge		US	

APPL-NO: 10/ 835517

DATE FILED: April 28, 2004

RELATED-US-APPL-DATA:

child 10835517 A1 20040428

parent continuation-of 08954771 19971020 US ABANDONED

child 08954771 19971020 US

parent continuation-of 08462386 19950605 US ABANDONED

child 08462386 19950605 US

parent continuation-in-part-of 08435093 19950504 US ABANDONED

child 08435093 19950504 US

parent continuation-in-part-of 08356060 19941214 US GRANTED

parent-patent 5844079 US

child 08356060 19941214 US

parent continuation-in-part-of 08176427 19931230 US GRANTED

parent-patent 5789543 US

US-CL-CURRENT: 514/12

ABSTRACT:

The present invention concerns the discovery that proteins encoded by a family of vertebrate genes, termed here hedgehog-related genes, comprise morphogenic signals produced by embryonic patterning centers, and are involved in the formation of ordered spatial arrangements of differentiated tissues in vertebrates. The present invention makes available compositions and methods that can be utilized, for example to generate and/or maintain an array of different vertebrate tissue both in vitro and in vivo.

RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. Ser. No. 08/435,093, filed May 4, 1995, which is a continuation-in-part of U.S. Ser. No. 08/356,060, filed Dec. 14, 1994, which is a continuation-in-part of U.S. Ser. No. 08/227,371 filed Dec. 30, 1993 and entitled "Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto", the teachings of which are incorporated herein by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (84):

[0144] When it is desirable to express only a portion of an hh protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20050003473

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050003473 A1

TITLE: Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase

PUBLICATION-DATE: January 6, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Bolten, Suzanne L.	Kirkwood	MO	US	
Clayton, Robert A.	Foristell	MO	US	
Easton, Alan M.	Maryland Heights	MO	US	
Engel, Leslie C.	Des Peres	MO	US	
Messing, Dean M.	St. Louis	MO	US	
Ng, John S.	Thousand Oaks	CA	US	
Reitz, Beverly	Chesterfield	MO	US	
Walker, Mark C.	Chesterfield	MO	US	
Wang, Ping T.	Chesterfield	MO	US	

APPL-NO: 10/ 900856

DATE FILED: July 28, 2004

RELATED-US-APPL-DATA:

child 10900856 A1 20040728

parent division-of 10021425 20011030 US PENDING

non-provisional-of-provisional 60244300 20001030 US

US-CL-CURRENT: 435/58, 435/189 , 435/254.3 , 435/320.1 , 435/59 , 536/23.2

ABSTRACT:

The present invention relates to a novel cytochrome P450-like enzyme (Aspergillus ochraceus 11 alpha hydroxylase) and an oxidoreductase (Aspergillus ochraceus oxidoreductase) isolated from cDNA library generated from the mRNA of Aspergillus ochraceus spores. When the cDNA encoding the 11 alpha hydroxylase was co-expressed in Spodoptera frugiperda (Sf-9) insect cells with the cDNA encoding human oxidoreductase as an electron donor, it successfully catalyzed the conversion of the steroid substrate 4-androstene-3,17-dione (AD) to 11 alpha-hydroxy-AD as determined by HPLC analysis. The invention also relates to nucleic acid molecules associated with or derived from these cDNAs including complements, homologues and fragments thereof, and methods of using these nucleic acid molecules, to generate, for example, polypeptides and fragments thereof. The invention also relates to the generation of antibodies that recognizes the A. ochraceus 11 alpha hydroxylase and oxidoreductase and methods of using these antibodies to detect the presence of these native and recombinant polypeptides within unmodified and transformed host cells, respectively. The invention also provides methods of expressing the Aspergillus 11 alpha hydroxylase gene separately, or in combination with human or Aspergillus oxidoreductase, in heterologous host cells, to facilitate the bioconversion of steroid substrates to their 11 alpha hydroxy-counterparts.

PRIORITY

[0001] The present application claims priority under Title 35, United States Code, .sctn. 119 of U.S. Provisional Application Ser. No. 60/244,300, filed Oct. 30, 2000.

---------- KWIC ---------

Detail Description Paragraph - DETX (27):

[0179] When expressed in the E. coli cytoplasm, the gene encoding the proteins of the present invention may also be constructed such that at the 5' end of the gene codons are added to encode Met.sup.-2-Ala.sup.-1, Met.sup.-2-Ser.sup.-1, Met.sup.-2-Cys.sup.-1, or Met.sup.-1 at the N-terminus of the protein. The N termini of proteins made in the cytoplasm of E. coli are affected by post-translational processing by methionine aminopeptidase (Ben Bassat et al., J. Bacteriol. 169:751-757, 1987), and possibly by other peptidases, so that upon expression the methionine is cleaved off the N-terminus. The proteins of the present invention may include polypeptides having Met.sup.-1, Ala.sup.-1, Ser.sup.-1, Cys.sup.-1, Met.sup.-2-Ala.sup.-1, Met.sup.-2-Ser.sup.-1, or Met.sup.-2-Cys.sup.-1 at the N-terminus. These mutant proteins may also be expressed in E. coli by fusing a secretion signal peptide to the N-terminus. This signal peptide is cleaved from the polypeptide as part of the secretion process.

PGPUB-DOCUMENT-NUMBER: 20040253615

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040253615 A1

TITLE: NOD nucleic acids and polypeptides

PUBLICATION-DATE: December 16, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Inohara, Naohiro	Ann Arbor	MI	US	
Nunez, Gabriel	Ann Arbor	MI	US	

APPL-NO: 10/ 794342

DATE FILED: March 5, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60452274 20030305 US

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/69.1 , 530/350 , 536/23.5

ABSTRACT:

The present invention relates to the NOD proteins and nucleic acids encoding the NOD proteins. The present invention further provides assays for the detection of NOD polymorphisms and mutations associated with disease states, as well as methods of screening for ligands and modulators of NOD proteins.

[0001] This application claims priority to provisional patent application Ser. No. 60/452,274, filed Mar. 5, 2004; which is herein incorporated by reference in its entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (129):

[0163] In addition, the present invention provides fragments of NOD polypeptides (i.e., truncation mutants). In some embodiments of the present invention, when expression of a portion of the NOD protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA 84:2718 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerivisiae), or in vitro by use of purified MAP.

PGPUB-DOCUMENT-NUMBER: 20040235739

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040235739 A1

TITLE: Neuroprotective methods and reagents

PUBLICATION-DATE: November 25, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Mahanthappa, Nagesh K.	Cambridge	MA	US	

APPL-NO: 10/ 849704

DATE FILED: May 19, 2004

RELATED-US-APPL-DATA:

child 10849704 A1 20040519

parent continuation-of 09418221 19991014 US GRANTED

parent-patent 6767888 US

child 09418221 19991014 US

parent continuation-in-part-of 08883656 19970627 US ABANDONED

US-CL-CURRENT: 514/12

ABSTRACT:

One aspect of the present application relates to a method for limiting damage to neuronal cells by ischemic or epoxic conditions, e.g., such as may be manifest by a reduction in brain infarct volume, by administering to an individual a hedgehog therapeutic or ptc therapeutic in an amount effective for reducing cerebral infarct volume.

[0001] This application is a continuation-in-part of U.S. patent application Ser. No. 08/883,656, filed Jun. 27, 1997, incorporated herein by reference in its entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (70):

[0110] When it is desirable to express only a portion of a hedgehog protein, such as a form lacking a portion of the N-terminus, i.e., a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro

activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040224882

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040224882 A1

TITLE: Vertebrate embryonic pattern inducing proteins and uses related thereto

PUBLICATION-DATE: November 11, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ingham, Philip W.	Summertown	MA	GB	
McMahon, Andrew P.	Lexington	MA	US	
Tabin, Clifford J.	Cambridge		US	

APPL-NO: 10/ 647654

DATE FILED: August 25, 2003

RELATED-US-APPL-DATA:

child 10647654 A1 20030825

parent continuation-of 08954128 19971020 US GRANTED

parent-patent 6610656 US

child 08954128 19971020 US

parent continuation-in-part-of 08435093 19950504 US ABANDONED

child 08435093 19950504 US

parent continuation-in-part-of 08356060 19941214 US GRANTED

parent-patent 5844079 US

child 08356060 19941214 US

parent continuation-in-part-of 08176427 19931230 US GRANTED

parent-patent 5789543 US

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US93/09945	1993WO-PCT/US93/09945	October 18, 1993

US-CL-CURRENT: 514/12, 435/325

ABSTRACT:

The present invention concerns the discovery that proteins encoded by a family of vertebrate genes, termed here hedgehog-related genes, comprise morphogenic signals produced by embryonic patterning centers, and are involved in the formation of ordered spatial arrangements of differentiated tissues in vertebrates. The present invention makes available compositions and methods

that can be utilized, for example to generate and/or maintain an array of different vertebrate tissue both in vitro and in vivo.

RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. Ser. No. 08/435,093, filed May 4, 1995, which is a continuation-in-part of U.S. Ser. No. 08/356,060, filed Dec. 14, 1994, which is a continuation-in-part of U.S. Ser. No. 08/227,371 filed Dec. 30, 1993"; and entitled "Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto", the teachings of which are incorporated herein by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (84):

[0144] When it is desirable to express only a portion of an hh protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well-known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040220096

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040220096 A1

TITLE: Method and compositions for treating dopaminergic and gabanergic disorders

PUBLICATION-DATE: November 4, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Galdes, Alphonse	Lexington	MA	US	
Mahanthappa, Nagesh	Cambridge	MA	US	
Engber, Thomas	Acton	MA	US	

APPL-NO: 10/ 665923

DATE FILED: September 18, 2003

RELATED-US-APPL-DATA:

child 10665923 A1 20030918

parent continuation-of 09325602 19990603 US ABANDONED

child 09325602 19990603 US

parent continuation-in-part-of 09238243 19990127 US ABANDONED

US-CL-CURRENT: 514/12

ABSTRACT:

It is shown here that hedgehog polypeptides possess novel activities beyond phenotype specification. Using cultures derived from the embryonic day 14.5 (E14.5) rat ventral mesencephalon, we show that hedgehog is also trophic for dopaminergic neurons and other neurons which are sensitive to exotoxicity.

RELATED APPLICATIONS

[0001] The present application is a continuation-in-part of U.S. Ser. No. 09/238,243, filed 27 Jan. 1999, the specification of which is incorporated by reference herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (132):

[0167] When it is desirable to express only a portion of a hedgehog polypeptide, such as a form lacking a portion of the N-terminus, i.e. a truncation **mutant** which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a **methionine** at the N-terminal position can be enzymatically cleaved by the use of the enzyme **methionine aminopeptidase** (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in

vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040208862

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040208862 A1

TITLE: Neuronal regeneration

PUBLICATION-DATE: October 21, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Brady-Kalnay, Susann	Cleveland Heights	OH	US	
Bellamkonda, Ravi V.	Marietta	GA	US	

APPL-NO: 10/ 754102

DATE FILED: January 7, 2004

RELATED-US-APPL-DATA:

child 10754102 A1 20040107

parent continuation-in-part-of PCT/US02/32942 20021015 US PENDING

non-provisional-of-provisional 60329155 20011012 US

US-CL-CURRENT: 424/94.6

ABSTRACT:

C1 activators and/or C2 inhibitors can promote neuronal regeneration, even in the presence of the proteoglycans which compose glial rich scar tissue. Accordingly, the methods of the present application can be used to overcome the inhibitory effects of glial rich scar tissue, and thus be used to promote neuronal regeneration following tissue injury and/or degeneration, including tissue injury or degeneration which results in formation of a glial rich scar. The methods of the present application thus provide a novel treatment option for patients afflicted with any of a number of conditions which result in injury or degeneration of neuronal cells of the central and peripheral nervous system. Examples of conditions which can be treated by the methods described herein include, without limitation, spinal cord injury, brain injury (following surgery, stroke, cancer treatment, or trauma), peripheral nerve injury, Parkinson's disease, Huntington's disease, detached retina, macular degeneration, Alzheimer's disease, amotrophic lateral sclerosis (ALS), multiple sclerosis, peripheral neuropathy, and diabetic neuropathy. One of skill in the art will appreciate that injuries or conditions that results in damage to or degeneration of neurons are candidates for treatment with the compositions of the present application.

RELATED APPLICATIONS

[0001] This application is a continuation-in-part of and claims priority to PCT/US02/32942, filed Oct. 15, 2002, and U.S. provisional application 60/329,155 filed Oct. 12, 2001, the disclosures of which are hereby incorporated by reference in their entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (152):

[0202] When it is desirable to express only a portion of a protein, such as a form lacking a portion of the N-terminus, e.g. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the enzyme methionine aminopeptidase (MAP).

PGPUB-DOCUMENT-NUMBER: 20040171546

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040171546 A1

TITLE: Regulation of lung tissue by hedgehog-like polypeptides and formulations and uses related thereto

PUBLICATION-DATE: September 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Pepicelli, Carmen V.	Lowell	MA	US	
Lewis, Paula M.	Cambridge	MA	US	
McMahon, Andrew P.	Lexington	MA	US	

APPL-NO: 10/ 727195

DATE FILED: December 3, 2003

RELATED-US-APPL-DATA:

child 10727195 A1 20031203

parent continuation-of 09394020 19990910 US ABANDONED

non-provisional-of-provisional 60099952 19980911 US

US-CL-CURRENT: 514/12

ABSTRACT:

The present application relates to a method for modulating the growth state of an lung tissue, or a cell thereof, e.g., by ectopically contacting the tissue, in vitro or in vivo, with a hedgehog therapeutic, a ptc therapeutic, or an FGF-10 therapeutic in an amount effective to alter the rate (promote or inhibit) of proliferation of cells in the lung tissue, e.g., relative to the absence of administeration of the hedgehog therapeutic or ptc therapeutic. The subject method can be used, for example, to modulate the growth state of epithelial and/or mesenchymal cells of a lung tissue, such as may be useful as part of a regimen for prevention of a disease state, or in the treatment of an existing disease state or other damage to the lung tissue.

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional application 60/099,952, filed Sep. 11, 1998 and entitled "Regulation of Lung Tissue by Hedgehog-like Polypeptides, and Formulations and Uses Related Thereto", the specification of which is incorporated by reference herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (70):

[0104] When it is desirable to express only a portion of an hedgehog protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon

(ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040171533

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040171533 A1

TITLE: Methods and compositions for regulating adiopocytes

PUBLICATION-DATE: September 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Zehentner, Barbara	Viecht		DE	
Leser-Reiff, Ulrike	Penzberg		DE	
Burtscher, Helmut	Habach		DE	

APPL-NO: 09/ 795917

DATE FILED: February 28, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60186058 20000229 US

US-CL-CURRENT: 514/12, 435/455

ABSTRACT:

The present application relates to a method for modulating the formation and/or maintenance of adipocyte tissue by ectopically contacting adipocyte cells, especially adipocyte stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic or ptc therapeutic in an amount effective to alter the growth state the treated cells, e.g., relative to the absence of administeration of the hedgehog therapeutic or ptc therapeutic.

REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 60/186,058, filed Feb. 29, 2000, the specification of which are herein incorporated by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (112):

[0128] When it is desirable to express only a portion of an hedgehog protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et

al., supra).

PGPUB-DOCUMENT-NUMBER: 20040171115

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040171115 A1

TITLE: Multi-functional hematopoietic fusion proteins between sequence rearranged G-CSF receptor agonists and other hematopoietic factors

PUBLICATION-DATE: September 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Feng, Yiqing	St. Louis	MO	US	
Staten, Nicholas R.	St. Louis	MO	US	
Baum, Charles M.	Evanston	IL	US	
Summers, Neena L.	St. Charles	MO	US	
Caparon, Maire Helena	Chesterfield	MO	US	
Bauer, S. Christopher	New Haven	MO	US	
Zurfluh, Linda L.	Kirkwood	MO	US	
McKearn, John P.	Glencoe	MO	US	
Klein, Barbara K.	St. Louis	MI	US	
Lee, Stephen C.	St. Louis	MO	US	
McWherter, Charles A.	Wildwood	MO	US	
Giri, Judith G.	Chesterfield	MO	US	

APPL-NO: 10/ 695584

DATE FILED: October 27, 2003

RELATED-US-APPL-DATA:

child 10695584 A1 20031027

parent continuation-of 09510238 20000222 US GRANTED

parent-patent 6730303 US

child 09510238 20000222 US

parent division-of 08835162 19970404 US GRANTED

parent-patent 6066318 US

child 08835162 19970404 US

parent continuation-in-part-of PCT/US96/15774 19961004 US PENDING

non-provisional-of-provisional 60004834 19951005 US

US-CL-CURRENT: 435/69.1, 435/320.1 , 435/325 , 530/350 , 536/23.5

ABSTRACT:

Disclosed are novel multi-functional hematopoietic receptor agonist proteins, DNAs which encode the multi-functional hematopoietic receptor agonists proteins, methods of making the multi-functional hematopoietic receptor

agonists proteins and methods of using the multi-functional hematopoietic receptor agonists proteins.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a continuation of U.S. patent application Ser. No. 09/510,238, filed Feb. 22, 2002, pending, which is a divisional of U.S. patent application Ser. No. 08/835,162 filed Apr. 4, 1997, now issued as U.S. Pat. No. 6,066,318 on May 23, 2000, which is a continuation-in-part of PCT/US 96/15774 filed Oct. 4, 1996 which claims priority under 35 U.S.C. .sctn.119(e) of U.S. Provisional Pat. App. Ser. No. 60/004,834, filed Oct. 5, 1995, now abandoned.

---------- KWIC --------

Detail Description Paragraph - DETX (42):

[0363] As another aspect of the present invention, there is provided a method for producing the novel multi-functional hematopoietic receptor agonists. The method of the present invention involves culturing suitable cells or cell line, which has been transformed with a vector containing a DNA sequence coding for expression of a novel multi-functional hematopoietic receptor agonist. Suitable cells or cell lines may be bacterial cells. For example, the various strains of E. coli are well-known as host cells in the field of biotechnology. Examples of such strains include E. coli strains JM101 (Yanish-Perron et al. Gene 33: 103-119, 1985) and MON105 (Obukowicz et al., Applied Environmental Microbiology 58: 1511-1523, 1992). Also included in the present invention is the expression of the multi-functional hematopoietic receptor agonist protein utilizing a chromosomal expression vector for E. coli based on the bacteriophage Mu (Weinberg et al., Gene 126: 25-33, 1993). Various strains of B. subtilis may also be employed in this method. Many strains of yeast cells known to those skilled in the art are also available as host cells for expression of the polypeptides of the present invention. When expressed in the E. coli cytoplasm, the gene encoding the multi-functional hematopoietic receptor agonists of the present invention may also be constructed such that at the 5' end of the gene codons are added to encode Met.sup.-2-Ala.sup.-1- or Met.sup.-1 at the N-terminus of the protein. The N termini of proteins made in the cytoplasm of E. coli are affected by post-translational processing by methionine aminopeptidase (Ben Bassat et al., J. Bac. 169:751-757, 1987) and possibly by other peptidases so that upon expression the methionine is cleaved off the N-terminus. The multi-functional hematopoietic receptor agonists of the present invention may include multi-functional hematopoietic receptor agonist polypeptides having Met.sup.-1, Ala.sup.-1 or Met.sup.-2-Ala.sup.-1 at the N-terminus. These mutant multi-functional hematopoietic receptor agonists may also be expressed in E. coli by fusing a secretion signal peptide to the N-terminus. This signal peptide is cleaved from the polypeptide as part of the secretion process.

PGPUB-DOCUMENT-NUMBER: 20040170969

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040170969 A1

TITLE: GRF2 binding proteins and applications thereof

PUBLICATION-DATE: September 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Moran, Michael F.	Toronto		CA	
Ornatsky, Olga	Richmond Hill		CA	
McBroom, Linda	Toronto		CA	

APPL-NO: 09/ 897787

DATE FILED: June 29, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60215504 20000630 US

non-provisional-of-provisional 60263690 20010124 US

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/69.7 , 530/399 , 536/23.5

ABSTRACT:

Reagents and methods of use thereof regarding proteins and complexes of GRF2-interacting proteins (GRF2-IP) and proteins interaction with GRF2-IP, as well as polynucleotides encoding those proteins.

REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to Provisional application 60/215,504, filed on Jun. 30, 2000, and of Provisional application 60/263,690, filed on Jan. 24, 2001, the specifications of which are incorporated by reference herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (110):

[0169] When expression of a carboxy terminal fragment of a full-length GRF2 pathway component is desired, i.e. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., (1987) PNAS USA 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al.).

PGPUB-DOCUMENT-NUMBER: 20040147469

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040147469 A1

TITLE: Methods of inhibiting glial scar formation

PUBLICATION-DATE: July 29, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Grimpe, Barbara	Cleveland	OH	US	
Silver, Jerry	Cleveland	OH	US	

APPL-NO: 10/ 698190

DATE FILED: October 31, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60423082 20021101 US

non-provisional-of-provisional 60471447 20030516 US

US-CL-CURRENT: 514/44

ABSTRACT:

The present invention provides methods and compositions for inhibiting glial scar formation, methods and compositions for decreasing GAG content, methods and composition for decreasing proteoglycan gene expression, and methods and compositions for promoting neuronal regeneration. The present invention further provides methods of identifying additional agents that inhibit glial scar formation and/or promote neuronal regeneration.

---------- KWIC ---------

Detail Description Paragraph - DETX (156):

[0204] When it is desirable to express only a portion of a protein, such as a form lacking a portion of the N-terminus, e.g. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the enzyme methionine aminopeptidase (MAP).

PGPUB-DOCUMENT-NUMBER: 20040146900

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040146900 A1

TITLE: Ataxia associated gene and protein

PUBLICATION-DATE: July 29, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Burmeister, Margit	Ann Arbor	MI	US	

APPL-NO: 10/ 699941

DATE FILED: November 3, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60422971 20021101 US

non-provisional-of-provisional 60424973 20021108 US

US-CL-CURRENT: 435/6, 435/7.2

ABSTRACT:

The present invention relates to ataxia, in particular to protein and nucleic acids encoding proteins associated with ataxia. The present invention provides assays for the detection of ataxia polymorphisms and mutations associated with disease or disease carrier states.

[0001] This application claims priority to provisional patent applications serial No. 60/422,971, filed Nov. 1, 2002 and 60/424,973, filed Nov. 8, 2002, each of which is herein incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (115):

[0138] In addition, the present invention provides fragments of Cayman ataxia (i.e., truncation mutants). In some embodiments of the present invention, when expression of a portion of the Cayman ataxia protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA 84:2718 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerivisiae), or in vitro by use of purified MAP.

PGPUB-DOCUMENT-NUMBER: 20040146879

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040146879 A1

TITLE: Novel human genes and gene expression products

PUBLICATION-DATE: July 29, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Astle, Jon H.	Taunton	MA	US	
Boardman, Lisa Allyn	Rochester	MN	US	
Burgart, Lawrence J.	Rochester	MN	US	
Burgess, Christopher C.	Westwood	MA	US	
Catino, Theodore J.	Attleboro	MA	US	
Dwivedi, Poornima	Alamo	CA	US	
Lewis, Marcia E.	Cohasset	MA	US	
Molino, Gary A.	Norfolk	MA	US	
Myerow, Susan H.	Lexington	MA	US	
Thiagalingam, Arunthathi	Lexington	MA	US	
Thibodeau, Stephen N.	Rochester	MN	US	

APPL-NO: 10/ 610049

DATE FILED: June 30, 2003

RELATED-US-APPL-DATA:

child 10610049 A1 20030630

parent continuation-in-part-of 09871161 20010531 US PENDING

child 09871161 20010531 US

parent continuation-of 09385982 19990830 US GRANTED

parent-patent 6262334 US

child 09871161 20010531 US

parent continuation-in-part-of 09328111 19990608 US GRANTED

parent-patent 6262333 US

non-provisional-of-provisional 60117393 19990127 US

non-provisional-of-provisional 60098639 19980831 US

US-CL-CURRENT: 435/6, 435/7.23

ABSTRACT:

This invention relates to novel human genes, to proteins expressed by the genes, and to variants of the proteins. The invention also relates to diagnostic assays and therapeutic agents related to the genes and proteins, including probes, antisense constructs, and antibodies. The subject nucleic

acids have been found to be differentially regulated in tumor cells, particularly in colon cancer tissue.

RELATED APPLICATION INFORMATION

[0001] This application is a continuation-in-part of application Ser. No. 09/871,161, filed on May 31, 2001, which is a continuation of application Ser. No. 09/385,982, filed on Aug. 30, 1999, now U.S. Pat. No. 6,262,334, which claims the benefit of Provisional Application No. 60/117,393, filed Jan. 27, 1999 and 60/098,639, filed Aug. 31, 1998, which is a continuation-in-part of 09/328,111, filed Jun. 8, 1999, now U.S. Pat. No. 6,262,333, which claims the benefit of Provisional Application No. 60/088,081, filed Jun. 10, 1998, all of which are incorporated by reference herein, in their entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (142):

[0173] When it is desirable to express only a portion of a gene, e.g., a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040142468

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040142468 A1

TITLE: Modulation of systemic immune responses by transplantation of hematopoietic stem cells transduced with genes encoding antigens and antigen presenting cell regulatory molecules

PUBLICATION-DATE: July 22, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Pardoll, Drew M	Brookeville	MD	US	
Cheng, Linzhao	Columbia	MD	US	
Cui, Yan	New Orleans	LA	US	
Civin, Curt I	Towson	MD	US	
Whartenby, Katherine	Baltimore	MD	US	

APPL-NO: 10/ 471559

DATE FILED: March 18, 2004

PCT-DATA:
APPL-NO: PCT/US02/08411
DATE-FILED: Mar 18, 2002
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 435/455

ABSTRACT:

The invention provides methods and compositions for the modulation of systemic immune responses by transplantation of hematopoietic stem cells transduced with genes encoding antigens and antigen presenting cell regulatory molecules. The invention includes bi-cistronic lentiviral expression vectors adapted for antigen expression in antigen presenting cells for use in DNA vaccines directed against pathogens and tumor antigens as well as for the treatment of autoimmune disease and for the establishment of antigen tolerance.

---------- KWIC ---------

Detail Description Paragraph - DETX (167):

[0189] When it is desirable to express only a portion of an Antigen protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro

activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal **methionine,** if desired, can be achieved either in vivo by expressing Antigen derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040132120

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040132120 A1

TITLE: Cell regulatory genes, encoded products, and uses related thereto

PUBLICATION-DATE: July 8, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Yang, Annie	Boston	MA	US	
McKeon, Frank	Boston	MA	US	

APPL-NO: 10/ 716359

DATE FILED: November 18, 2003

RELATED-US-APPL-DATA:

child 10716359 A1 20031118

parent continuation-of 09174493 19981015 US PENDING

non-provisional-of-provisional 60087216 19980529 US

non-provisional-of-provisional 60062076 19971015 US

US-CL-CURRENT: 435/7.23, 424/146.1 , 530/388.26

ABSTRACT:

This application describes the cloning of p63, a gene at chromosome 3q27-29, that bears homology to the tumor suppressor p53. The p63 gene encodes at least six different isotypes. p63 was detected in a variety of human and mouse tissue and demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Isotopes of p63 lacking a transactivation domain act as dominant negatives towards the transactivation by p53 and p63.

---------- KWIC ---------

Detail Description Paragraph - DETX (110):

[0192] When it is desirable to express only a portion of a p63 protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing p63 derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified

MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040131599

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040131599 A1

TITLE: Fas ligand expressing hematopoietic cells for transplantation

PUBLICATION-DATE: July 8, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Civin, Curt I	Towson	MD	US	
Drachman, Daniel	Stevenson	MD	US	
Whartenby, Katherine	Baltimore	MD	US	
Pardoll, Drew M	Brookville	MD	US	

APPL-NO: 10/ 471881

DATE FILED: February 25, 2004

PCT-DATA:
APPL-NO: PCT/US02/07861
DATE-FILED: Mar 13, 2002
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 424/93.21, 435/372

ABSTRACT:

The invention provides methods and compositions utilizing FasL armed donor graft cells to reduce or eliminate host allogeneic or xenogeneic graft rejection, and FasL armed host cells to reduce or eliminate graft versus host disease.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 60/275,615, filed Mar. 13, 2001, the contents of which are specifically incorporated herein.

---------- KWIC ---------

Detail Description Paragraph - DETX (163):
[0212] When it is desirable to express only a portion of an FasL protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro

activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing FasL derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040127682

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040127682 A1

TITLE: Immunotoxin fusion proteins and means for expression thereof

PUBLICATION-DATE: July 1, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Neville, David M	Bethesda	MD	US	
Thompson, Jerry T	Frenchville	PA	US	
Hu, Huaizhong	Madison	WI	US	
Woo, Jung-Hee	Rockville	MD	US	
Ma, Shenglin	Indianapolis	IN	US	
Hexham, Jonathan Mark	S Orange	NJ	US	
Digan, Mary Ellen	Winchester	MA	US	

APPL-NO: 10/ 296085

DATE FILED: January 13, 2004

PCT-DATA:
APPL-NO: PCT/US01/16125
DATE-FILED: May 18, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 530/350

ABSTRACT:

The present invention described and shown in the specification and drawings provides novel recombinant DT-based immunotoxins, and, more specifically anti-T cell immunotoxin fusion proteins. Also provided are immunotoxins that can be expressed in bacterial, yeast, or mammalian cells. The invention also provides means for expression of the immunotoxin fusion protein. It is emphasized that this abstract is provided to comply with the rules requiring an abstract that will allow a searcher or other reader to quickly ascertain the subject matter of the technical disclosure. It is submitted with the understanding that it will not be used to interpret or limit the scope or meaning of the claims.

---------- KWIC --------

Detail Description Paragraph - DETX (564):
[0555] The production and regulatory approval processes for biopharmaceuticals require detailed characterization of potential products. Therapeutic proteins should preferably be homogeneous, although limited, reproducible heterogeneity may be tolerated. Mass spectroscopy and N-terminal sequencing by Edman degradation revealed that the diphtheria toxin-based DT389-scFv(UCHT1) immunotoxin molecule expressed in E. coli and purified

following refolding was heterogeneous at the N-terminus, containing species both with (60%) and without (40%) the initiator methionine. Similar results were obtained with refolded, active material and inclusion bodies, produced at the laboratory scale and larger batches from high density fermentation. In an attempt to generate an N-terminally homogeneous molecule, a panel of seven N-terminal variants was designed, based on the specificity of bacterial methionine aminopeptidase (MAP) (Ben-Bassat, Bioprocess Technol. 12:147-59) (1991); Ben-Bassat et al. J. Bacteriol. 169:751-757; Gonzales and Robert-Baudouy, Microbiol. Revs. 18:319-344). The first residue immediately after the methionine has been shown to be the most important factor in efficiency of cleavage by MAP. In general, peptides with smaller amino acids (e.g. glycine, alanine, proline and serine) at this position constituted better substrates for MAP. In contrast, peptides with larger amino acids such as phenylalanine, leucine, methionine, glutamic acid, arginine or lysine, following the methionine, were poor substrates for MAP. Variable cleavage of methionine was observed whdn the intermediate-sized amino acids isoleucine, valine, cysteine and threonine were present at this position in the sequence. Mutants of DT389-scFv(UCHT1) were designed as good or poor substrates based on these data, and relatively conservative amino acid changes from the native diphtheria toxin sequence were chosen. See Table 17.

PGPUB-DOCUMENT-NUMBER: 20040110668

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040110668 A1

TITLE: Nucleic acid sequences differentially expressed in cancer tissue

PUBLICATION-DATE: June 10, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Burgess, Christopher C.	Westwood	MA	US	
Astle, Jon H.	Taunton	MA	US	
Carroll, Eddie III	Norwood	MA	US	
Catino, Theodore J.	Attleboro	MA	US	
Dwivedi, Poornima	Alamo	CA	US	
Molino, Gary A.	Norfolk	MA	US	
Thiagalingam, Arunthathi	Lexington	MA	US	
Lewis, Marcia E.	Cohasset	MA	US	

APPL-NO: 09/ 969034

DATE FILED: October 2, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60237271 20001002 US

US-CL-CURRENT: 514/12, 435/320.1 , 435/325 , 435/6 , 435/69.1 , 530/350 , 536/23.5 , 800/8

ABSTRACT:

This invention relates to novel nucleic acid sequences which are differentially expressed in cancer cells. The invention also relates to proteins and peptides encoded by the sequences, to diagnostic assays and therapeutic agents based on the sequences and proteins, and to probes, antisense constructs, and antibodies derived from the sequences and proteins or peptides. The subject nucleic acids have been found to be differentially expressed by tumor cells, particularly in colon cancer tissue.

[0001] This application claims priority Under 35 U.S.C. .sctn.119(e) from U.S. application No. 60/237,271, filed Oct. 2, 2000.

---------- KWIC ---------

Detail Description Paragraph - DETX (140):

[0170] When it is desirable to express only a portion of a gene, e.g., a truncation **mutant**, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a **methionine** at the N-terminal position can be enzymatically cleaved by the use of the enzyme **methionine aminopeptidase** (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., (1987) J. Bacteriol.

169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

PGPUB-DOCUMENT-NUMBER: 20040096922

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040096922 A1

TITLE: NPHP nucleic acids and proteins

PUBLICATION-DATE: May 20, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Hildebrandt, Friedhelm	Ann Arbor	MI	US	
Otto, Edgar	Ann Arbor	MI	US	
Hoefele, Julia	Ann Arbor	MI	US	
Ruf, Rainer	Ann Arbor	MI	US	
Mueller, Adelheid M.	Ann Arbor	MI	US	
Hiller, Karl S.	Ann Arbor	MI	US	
Wolf, Matthias T.F.	Ann Arbor	MI	US	
Schuermann, Maria J.	Nottuln		DE	
Becker, Achim	Herrenberg		DE	

APPL-NO: 10/ 648512

DATE FILED: August 26, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60406001 20020826 US

US-CL-CURRENT: 435/7.92

ABSTRACT:

The present invention relates to Nephronophthisis, in particular to the NPHP4 protein (nephroretinin or nephrocystin-4) and nucleic acids encoding the NPHP4 protein. The present invention also provides assays for the detection of NPHP4, and assays for detecting nephroretinin and inversin polymorphisms and mutations associated with disease states.

[0001] The present invention claims priority to U.S. Provisional Patent Application Serial No. 60/406,001, filed Aug. 26, 2002, the disclosure of which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (128):

[0164] In addition, the present invention provides fragments of NPHP4 (i.e., truncation mutants, e.g., SEQ ID NOs: 6, 10, 12, 14, 16, and 20). As described above, truncations of NPHP4 were found in families with NPHP type 4 disease. In some embodiments of the present invention, when expression of a portion of the NPHP4 protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP).

MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA 84:2718 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerivisiae), or in vitro by use of purified MAP.

PGPUB-DOCUMENT-NUMBER: 20040088752

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040088752 A1

TITLE: Divinyl ether synthase gene, and protein and uses thereof

PUBLICATION-DATE: May 6, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Howe, Gregg A.	East Lansing	MI	US	
Itoh, Aya	Tsuruoka-city		JP	

APPL-NO: 10/ 381870

DATE FILED: November 17, 2003

PCT-DATA:
APPL-NO: PCT/US01/31296
DATE-FILED: Oct 5, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 800/278, 435/193 , 435/320.1 , 435/419 , 435/69.1 , 536/23.2 , 800/286

ABSTRACT:

The present invention relates to divinyl ether synthase genes, proteins, and methods of their use. The present invention encompasses both native and recombinant wild-type forms of the synthase, as well as mutants and variant forms, some of which possess altered characteristics relative to the wild-type synthase. The present invention also relates to methods of using divinyl ether synthase genes and proteins, including in their expression in transgenic organisms and in the production of divinyl ether fatty acids, and to methods of suing divinyl ether fatty acids, including in the protection of plants from pathogens.

[0001] This application claims priority to U.S. Provisional Application Serial No. 60/238,415, filed on Oct. 6, 2000.

---------- KWIC ---------

Detail Description Paragraph - DETX (137):
[0174] In addition, the present invention provides isolated nucleic acid sequences encoding fragments of DES (i.e., truncation mutants), and the polypeptides encoded by such nucleic acid sequences. In preferred embodiments, the DES fragment is biologically active. In some embodiments of the present invention, when expression of a portion of a DES protein is desired, it may be

necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (AP). MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751-757 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA, 84:2718-1722 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host that produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP.

PGPUB-DOCUMENT-NUMBER: 20040077020

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040077020 A1

TITLE: Diagnostic microarray for inflammatory bowel disease, crohn's disease and ulcerative colitis

PUBLICATION-DATE: April 22, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Mannick, Elizabeth E.	New Orleans	LA	US	
Liu, Zhiyun	Houston	TX	US	
Serrano, Maria-Stella	River Ridge	LA	US	

APPL-NO: 10/ 432785

DATE FILED: November 20, 2003

PCT-DATA:
APPL-NO: PCT/US01/45096
DATE-FILED: Nov 30, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 435/7.1

ABSTRACT:

Using RNA samples from mononuclear blood cells, gene sequences were identified that can be used to identify patients with IBD, and then distinguish patients with Crohn's disease from those with ulcerative colitis. Sequences were identified whose overexpression was distinct to patients with IBD, Crohn's disease, and ulcerative colitis when compared to patients with non-IBD intestinal disorders. Additionally, cluster analysis was used to identify twenty-five sequences that are IBD-related, and whose transcription pattern can be used in a microarray analysis to identify patients with IBD with a sensitivity of 84% and a specificity of 100%. Cluster analysis also identified thirty-six genes that could be used to distinguish patients with Crohn's disease from those with ulcerative colitis with a sensitivity of 89% and a specificity of 80%.

[0001] The benefit of the filing dates of provisional applications Nos. 60/286,602 filed Apr. 26, 2001, 60/264,909 filed Jan. 29, 2001, and 60/250,303 filed Nov. 30, 2000 are claimed under 35 U.S.C. .sctn. 119(e) in the United States, and are claimed under applicable treaties and conventions in all countries.

---------- KWIC --------

Detail Description Table CWU - DETL (1):

1TABLE 1 Gene Expression in Fourteen Patients with Crohn's Disease Sequence ID with Genbank Accession # in Parentheses CD Median Overexpressed Genes in Crohn's Disease Messenger RNA for beta-globin (Acc# M34539) 3.41 mRNA for brain acyl-CoA hydrolase (Acc# D88894) 1.91 Breast epithelial antigen BA46 (Acc# U58516) 1.83 Ribosomal protein (Acc# M15661) 1.83 MOP4 (Acc# U51625) 1.79 Tristetraproline (TTP) (Acc# M63625) 1.79 atrophin-1 related protein (Acc# AF001845) 1.78 mRNA for hepatoma-derived growth factor (Acc# D16431) 1.78 Fatty acid binding protein homologue (PA-FABP) (Acc# M94856) 1.75 Tumorous imaginal discs protein Tid56 homolog (TID1) (Acc# AF061749) 1.75 Cellular growth-regulating protein (Acc# L10844) 1.75 Armadillo repeat protein (Acc# U51269). 1.73 Messenger RNA for alpha globin (Acc# V00493) 1.72 Protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) (Acc# U48296) 1.68 Nicotinic acetylcholine receptor alpha3 subunit precursor (Acc# U6243) 1.67 mRNA for brain cholecystokinin receptor (Acc# D13305) 1.66 Hom. of Drosophila splicing regulator suppressor-of-white-apricot (Acc# U08377) 1.65 Muscle glycogen synthase (Acc# J04501) 1.64 mRNA for MAT8 protein (Acc# X93036) 1.62 jun-B mRNA for JUN-B protein (Acc# X51345) 1.62 Acidic calponin (Acc# S80562) 1.61 Type 1 neurofibromatosis protein (Acc# M82814) 1.61 mRNA for proton-ATPase-like protein (Acc# D89052) 1.60 Ribosomal protein S20 (RPS20) (Acc# L06498) 1.60 MRNA for S100 alpha protein (Acc# X58079) 1.58 Underexpressed Genes in Crohn's Disease Adult skeletal muscle alpha-actin mRNA (Acc# J00068) 0.17 mRNA for vascular smooth muscle alpha-actin (Acc# X13839) 0.21 mRNA for enteric smooth muscle gamma-actin (Acc# X16940) 0.22 MHC class I HLA-C-alpha-2 chain and alternative, clones 4 and 10 (Acc# M24097) 0.23 mRNA for beta-actin (Acc# AB004047) 0.23 mRNA for HLA-Cw*0704 (Acc# X83394) 0.23 ACTB mRNA for mutant beta-actin (beta'-actin) (Acc# X63432) 0.25 Wnt-13 mRNA (Acc# Z71621) 0.25 mRNA for immunoglobulin kappa light chain (Acc# Y14736) 0.28 mRNA for HLA class-I (HLA-A26) heavy chain (clone cMIY-2) (Acc# D32130) 0.29 mRNA for HLA-DR antigens associated invariant chain (p33) (Acc# X00497) 0.29 MHC HLA-B39 (Acc# L42024) 0.30 Class II histocompatibility antigen beta-chain (pII-beta-3) (Acc# X00699) 0.30 mRNA for seryl-tRNA synthetase (Acc# X91257) 0.31 mRNA for KIAA0391 gene (Acc# AB002389) 0.32 mRNA for cytoskeletal gamma-actin (Acc# X04098) 0.34 Methionine aminopeptidase (Acc# U29607) 0.37 Epidermal growth factor receptor substrate (eps15) (Acc# U07707) 0.38 mRNA for ribosomal protein L3 (Acc# X73460) 0.38 Brain-expressed HHCPA78 homolog (Acc# X73591) 0.39 Wilm's tumor-related protein (QM) (Acc# M64241) 0.40 mRNA for B120 (Acc# AB001895) 0.40 mRNA for RAB7 protein (Acc# X93499) 0.40 Sigma receptor (Acc# U75283) 0.41 mRNA for ribosomal protein L14 (Acc# D87735) 0.41

US-PAT-NO: 6858391

DOCUMENT-IDENTIFIER: US 6858391 B2

TITLE: Nod2 nucleic acids and proteins

DATE-ISSUED: February 22, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Nunez; Gabriel	Ann Arbor	MI	N/A	N/A
Inohara; Naohiro	Ann Arbor	MI	N/A	N/A
Ogura; Yasunori	Ann Arbor	MI	N/A	N/A
Cho; Judy	Chicago	IL	N/A	N/A
Nicolae; Dan L.	Chicago	IL	N/A	N/A
Bonen; Denise	Chicago	IL	N/A	N/A

APPL-NO: 10/ 002974

DATE FILED: October 26, 2001

PARENT-CASE:

This application claims priority to U.S. provisional patent applications Ser. Nos. 60/244,266, filed Oct. 30, 2000 and 60/286,316, filed Apr. 25, 2001, each of which is herein incorporated by reference in its entirety. This patent application was supported in part by grant CA-64556 from the National Institutes of Health. The government has certain rights in the invention.

US-CL-CURRENT: 435/6, 435/91.1 , 435/91.2 , 536/23.1 , 536/24.3

ABSTRACT:

The present invention relates to intracellular signalling molecules, in particular the Nod2 protein and nucleic acids encoding the Nod2 protein. The present invention provides isolated nucleotide sequence encoding Nod2, isolated Nod2 peptides, antibodies that specifically bind Nod2, methods for the detection of Nod2, and methods for screening compounds for the ability to alter Nod2 associated signal transduction. The present invention also provides Nod2 variant alleles. The present invention further provides methods of identifying individuals at increased risk of developing Crohn's disease.

4 Claims, 44 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 49

---------- KWIC ---------

Detailed Description Text - DETX (141):

In addition, the present invention provides fragments of Nod2 (i.e., truncation mutants, e.g., SEQ ID NO:3). In some embodiments of the present invention, when expression of a portion of the Nod2 protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art

that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA 84:2718 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP.

US-PAT-NO: 6835815

DOCUMENT-IDENTIFIER: US 6835815 B2

TITLE: Nod2 nucleic acids and proteins

DATE-ISSUED: December 28, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Nunez; Gabriel	Ann Arbor	MI	N/A	N/A
Inohara; Naohiro	Ann Arbor	MI	N/A	N/A
Ogura; Yasunori	Ann Arbor	MI	N/A	N/A

APPL-NO: 10/ 014269

DATE FILED: October 26, 2001

PARENT-CASE:

This application claims priority to U.S. provisional patent application Ser. No. 60/244,289 filed Oct. 30, 2000, which is herein incorporated by reference in its entirety. This patent application was supported in part by grant CA-64556 from the National Institutes of Health. The government has certain rights in the invention.

US-CL-CURRENT: 530/350

ABSTRACT:

The present invention relates to intracellular signalling molecules, in particular the Nod2 protein and nucleic acids encoding the Nod2 protein. The present invention provides isolated nucleotide sequence encoding Nod2, isolated Nod2 peptides, antibodies that specifically bind Nod2, methods for the detection of Nod2, and methods for screening compounds for the ability to alter Nod2 associated signal transduction.

9 Claims, 16 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 21

---------- KWIC ---------

Detailed Description Text - DETX (132):

In addition, the present invention provides fragments of Nod2 (i.e., truncation mutants, e.g., SEQ ID NO:3). In some embodiments of the present invention, when expression of a portion of the Nod2 protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., J. Bacteriol., 169:751-757 [1987]) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al., Proc. Natl. Acad. Sci. USA

84:2718-1722 [1990]). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP.

US-PAT-NO: 6833239

DOCUMENT-IDENTIFIER: US 6833239 B1

TITLE: Methods to identify modulators of FKHL7 DNA-binding activity

DATE-ISSUED: December 21, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Sheffield; Val C.	Coralville	IA	N/A	N/A
Alward; Wallace L. M.	Iowa City	IA	N/A	N/A
Stone; Edwin M.	Iowa City	IA	N/A	N/A
Nishimura; Darryl	Coralville	IA	N/A	N/A
Patil; Shiva	Iowa City	IA	N/A	N/A

APPL-NO: 09/ 612809

DATE FILED: July 10, 2000

PARENT-CASE:

This application is a divisional application based on U.S. Ser. No. 09/083,351, filed on May 22, 1998 and now U.S. Pat. No. 6,087,107, which itself claims priority to provisional patent application 60/081,870, filed Apr. 15, 1998 and now abandoned.

US-CL-CURRENT: 435/6, 435/235.1 , 435/320.1 , 435/4 , 435/69.1 , 435/7.1 , 530/350 , 536/23.1 , 536/24.1

ABSTRACT:

Methods and compositions for treating a congenital heart disease and methods and compositions for prognosing or diagnosing a congenital heart disease in a subject are disclosed.

12 Claims, 4 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 4

---------- KWIC ---------

Detailed Description Text - DETX (101):

When it is desirable to express only a portion of an FKHL7 protein, such as a form lacking a portion of the N-terminus, i.e. a truncation **mutant** which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a **methionine** at the N-terminal position can be enzymatically cleaved by the use of the enzyme **methionine aminopeptidase** (MAP). MAP has been cloned from E. coli (Ben-Bassat et al (1987) J. Bacteriol 169 751-757) and Salmonella typhimurium and its in vitro) activity has been demonstrated oil recombinant proteins (Miller et al. (I 987) PNAS 84:2718-1722). Therefore, removal of an N-terminal **methionine,** if desired, can

be achieved either in vivo by expressing FKHL7 derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

US-PAT-NO: 6822071

DOCUMENT-IDENTIFIER: US 6822071 B1

TITLE: Polypeptides from Chlamydia pneumoniae and their use in the diagnosis, prevention and treatment of disease

DATE-ISSUED: November 23, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Stephens; Richard S.	Orinda	CA	N/A	N/A
Mitchell; Wayne	San Francsico	CA	N/A	N/A
Kalman; Sue S.	Saratoga	CA	N/A	N/A
Davis; Ronald	Palo Alto	CA	N/A	N/A

APPL-NO: 09/ 438185

DATE FILED: November 11, 1999

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to No. 60/128,606, filed Apr. 8, 1999 and No. 60/108,279, filed Nov. 12, 1998, which are incorporated herein by reference.

US-CL-CURRENT: 530/300, 530/350 , 530/402 , 530/810 , 530/811 , 530/812 , 530/813 , 530/814 , 530/820 , 530/825

ABSTRACT:

Chlamydia pneumoniae polypeptides are provided. The C. pneumoniae polypeptides can be used to prepare pharmaceutical compositions for the treatment or prevention of disease. In addition, the proteins can be used in methods for the diagnosis of C. pneumoniae infection.

6 Claims, 0 Drawing figures

Exemplary Claim Number: 1

---------- KWIC --------

Detailed Description Paragraph Table - DETL (11):

1012 (CT854) yzcB ABC Transporter Permease 0868 (CT727) mtA Metal Transport P-type ATPase 0279 Possible ABC Transporter Permease Protein 0543 (CT417) (Metal Transport Protein) 0692 (CT684) ABC Transporter 0542 (CT416) ABC Transporter ATPase 0690 (CT686) ABC Transporter Membrane Protein 0541 (CT415) solute binding protein Type-III Secretion 0323 (CT090) lcrD Low Calcium Response D 0324 (CT089) lcrE Low Calcium Response E 0811 (CT576) lcrH_1 Low Ca Response Protein H_1 1021 (CT862) lcrH_2 Low Calcium Response_2 0325 (CT088) sycE Secretion Chaperone 0702 (CT674) yscC Yop C/Gen Secretion Protein D 0828 (CT559) yscJ Yop Translocation J 0826 (CT561) yscL Yop Translocation L 0707 (CT669) yscN Yop N (Flagellar-Type ATPase) 0825 (CT562) yscR Yop Translocation R 0824 (CT563) yscS YopS Translocation Protein 0823 (CT564)

yscT YopT Translocation T 0322 (CT091) ytcU Yop Translocation Protein U Central Intermediary Metabolism Glycogen Metabolism 0856 (CT715) UDP-Glucose Pyrophosphorylase 0948 (CT798) glgA Glycogen Synthase 0475 (CT866) glgB Glucan Branching Enzyme 0607 (CT489) glgC Glucose-1-P Adenyltransferase 0307 (CT248) glgP Glycogen Phosphorylase 0388 (CT042) glgX Glycogen Hydrolase (debranching) 0326 (CT087) malQ Glucanotransferase 0851 (CT710) pckA Phosphoenolpyruvate Carboxykinase Phosphorous & Sulfur 0548 (CT435) cysI Sulfite Reductase 0920 (CT774) cysQ Sulfite Synthesis/Biphosphate Phosphatase 0025 (CT346) atsA Sulphohydrolase 0918 (CT772) ppa Inorganic Pyrophosphatase DNA Replication, Modification, Repair & Recombination DNA Mismatch Repair 0505 3-Methyladenine DNA Glycosylase 0812 (CT575) mutL DNA Mismatch Repair 0941 (CT792) mutS DNA Mismatch Repair 0402 (CT107) mutY Adenine Glycosylase 0732 (CT625) nfo Endonuclease IV 0837 (CT697) nth Endonuclease III DNA Modification 0596 (CT477) ada Methyltransferase 0114 (CT024) hemK A/G-specific Methylase 0891 (CT748) mfd Transcription-Repair Coupling 0620 (CT501) ruvA Holliday Junction Helicase 0390 (CT040) ruvB Holliday Junction Helicase 0621 (CT502) ruvC Crossover Junction Endonuclease 0053 (CT298) sms Sms Protein 0773 (CT607) ung Uracil DNA Glycosylase 1062 (CT329) xscA Exodosyribonuclease VII DNA Recombination 0762 (CT650) recA RecA Recombination Protein 0738 (CT639) recB Exodeoxyribonuclease V, Beta 0737 (CT640) recC Exodeoxyribonuclease V, Gamma 0123 (CT033) recD_1 Exodeoxyribonuclease V (Alpha Subunit)_1 0752 (CT652) recD_2 Exodeoxyribonuclease V, Alpha_2 0339 (CT074) recF ABC Superfamily ATPase 0340 (CT074) (frame-shift with 0339) 0563 (CT447) recJ ssDNA Exonuclease 0299 (CT240) recR Recombination Protein DNA Replication 0309 (CT250) dnaA_1 Replication Initiation Protein_1 0424 (CT275) dnaA_2 Replication Initiation Factor_2 0616 (CT497) dnaB Replicative DNA Helicase 0666 (CT545) dnaE DNA Pol III Alpha 0942 (CT794) dnaG DNA Primase 0338 (CT075) dnaN DNA Pol III (Beta) 0410 (CT261) dnaQ_1 DNA Pol III Epsilon Chain_1 0655 (CT536) dnaQ_2 DNA Pol III Epsilon Chain_2 0040 (CT334) dnaX_1 DNA Pol III Gamma and Tau_1 0272 (CT187) dnaX_2 DNA Pol III Gamma and Tau_2 0149 (CT146) dnU DNA Ligase 0274 (CT189) gyrA_1 DNA Gyrase Subunit A_1 0716 (CT660) gyrA_2 DNA Gyrase Subunit A_2 0275 (CT190) gyrB_1 DNA Gyrase Subunit B_1 0715 (CT661) gyrB_2 DNA Gyrase Subunit B_2 0416 (CT267) himD Integration Host Factor Alpha 0612 (CT493) polA DNA Polymerase I 0924 (CT778) priA Primosomal Protein N 0386 (CT044) ssb SS DNA Binding Protein 0835 (CT555) SWI/SNF family helicase_1 0849 (CT708) SWI/SNF family helicase_2 0769 (CT643) topA DNA Topoisomerase I-Fused to SWI Domain 0024 (CT347) xerC Integrase/recombinase 1024 (CT864) xerD Integrase/recombinase Eukaryotic-Type Chromatin Factors 0886 (CT743) hctA Histone-Like Developmental Protein 0384 (CT046) hctB Histone-like Protein 2 0878 (CT737) SET Domain protein 0577 (CT460) SWIB (YM74) Complex Protein UVR Exinuclease Repair System 0096 (CT333) uvrA Excinuclease ABC Subunit A 0801 (CT556) uvrB Excinuclease ABC Subunit B 0940 (CT791) uvrC Excinuclease ABC Subunit C 0772 (CT608) uvrD DNA Helicase Energy Metabolism Aerobic 0855 (CT714) gpdA Glycerol-3-P Dehydrogenase 0743 (CT634) nqrA Ubiquinone Oxidoreductase, Alpha 0427 (CT278) nqr2 NADH (Ubiquinone) Dehydrogenase 0428 (CT279) nqr3 NADH (Ubiquinone) Oxidoreductase, Gamma 0429 (CT280) nqr4 NADH (Ubiquinone) Reductase 4 0430 (CT281) nqr5 NADH (Ubiquinone) Reductase 5 0883 (CT740) nqr6 Phenolhydrolase/NADH (Ubiquinone) Oxidoreductase 6 ATP Biogenesis and metabolism 0351 (CT065) adt_1 ADP/ATP Translocase_1 0614 (CT495) adt_2 ADP/ATP Translocase_2 0088 (CT308) atpA ATP Synthase Subunit A 0089 (CT307) atpB ATP Synthase Subunit B 0090 (CT306) atpD ATP Synthase Subunit D 0086 (CT310) atpE ATP Synthase Subunit E 0091 (CT305) atpI ATP Synthase Subunit I 0092 (CT304) atpK ATP Synthase Subunit K 0860 (CT719) 0iF Flagellar M-Ring Protein Electron Transport Chain 0102 (CT013) cydA Cytochrome Oxidase Subunit I 0103 (CT014) cydB Cytochrome Oxidase Subunit II 0364 (CT059) Ferredoxin 0084 (CT312) Predicted Ferredoxin Glycolysis & Gluconeogenesis 0281 (CT215) dhnA Predicted 1,6-Fructose Biphosphate Aldolase 0800 (CT587) eno Enolase 0624 (CT505) gapA Glyceraldehyde-3-P Dehydrogenase

0056 (CT295) mrsA Phosphomannomutase 0967 (CT815) pgm Phosphoglucomutase 0160 (CT207) pfkA_1 Fructose-6-P Phosphotransferase_1 0208 (CT205) pfkA_2 Fructose-6-P Phosphotransferase_2 1025 (CT378) pgi Glucose-6-P Isomerase 0679 (CT693) pgk Phosphoglycerate Kinase 0863 (CT722) pgmA Phosphoglycerate Mutase 0097 (CT332) pyk Pyruvate Kinase 1063 (CT328) tpiS Triosephosphate Isomerase Pentose Phosphate Pathway 0239 (CT186) devB Glucose-6-P Dehydrogenase (DevB family) 1060 (CT331) dxs Transketolase 0360 (CT063) gnd 6-Phosphogluconate Dehydrogenase 0185 (CT121) rpe Ribulose-P Epimerase 0141 (CT213) rpiA Ribose-5-P Isomerase A 0083 (CT313) tal Transaldolase 0893 (CT750) tktB Transketolase 0238 (CT185) zwf Glucose-6-P Dehydrogenase Pyruvate Dehydrogenase 0833 (CT557) lpdA Lipoamide Dehydrogenase 0436 (CT285) lplA_1 Lipoate Protein Ligase-Like Protein 0618 (CT499) lplA_2 Lipoate-Protein Ligase A 0033 (CT340) pdhA&B Oxoisovalerate Dehydrogenase .alpha./.beta. Fusion 0304 (CT245) pdhA Pyruvate Dehydrogenase Alpha 0305 (CT246) pdhB Pyruvate Dehydrogenase Beta 0306 (CT247) pdhC Dihydrolipoamide Acetyltransferase TCA Cycle 0495 (CT390) aspC Aspartate Aminotransferase 1013 (CT855) fumC Fumarate Hydratase 1028 (CT376) mdhC Malate Dehydrogenase 0789 (CT592) sdhA Succinate Dehydrogenase 0790 (CT591) sdhB Succinate Dehydrogenase 0788 (CT593) sdhC Succinate Dehydrogenase 0378 (CT054) sucA Oxoglutarate Dehydrogenase 0377 (CT055) sucB_1 Dihydrolipoamide Succinyltransferase_1 0527 (CT400) sucB_2 Dihydrolipoamide Succinyltransferase_2 0973 (CT821) sucC Succinyl-CoA Synthetase, Beta 0974 (CT822) sucD Succinyl-CoA Synthetase, Alpha Protein Folding, Assembly & Modification Chaperones 0949 (CT799) ctc General Stress Protein 0534 (CT407) dksA DnaK Suppressor 0032 (CT341) dnaJ Heat Shock Protein J 0503 (CT396) dnaK Hsp-70 0134 (CT110) groEL_1 Hsp-60_1 0777 (CT604) groEL_2 Hsp-60_2 0898 (CT755) groEL_3 Hsp-60_3 0135 (CT111) groES 10 KDa Chaperonia 0502 (CT395) grpE HSP-70 Cofactor 0661 (CT541) mip FKBP-type Peptidyl-prolyl Cis-Trans Isomerase Proteases 0144 (CT113) clpB Clp Protease ATPase 0437 (CT286) clpC ClpC Protease 0520 (CT431) clpP_1 CLP Protease 0847 (CT706) clpP_2 CLP Protease Subunit 0846 (CT705) clpX CLP Protease ATPase 0269 (CT138) Dipeptidase 0998 (CT841) ftsH ATP-dependent Zinc Protease 0030 (CT343) gcp_1 O-Sialoglycoprotein Endopeptidase_1 0194 (CT197) gcp_2 O-Sialoglycoprotein Endopeptidase_2 0979 (CT823) htrA DO Serine Protease 0957 (CT806) ide Insulinase family/Protease III 0027 (CT344) lon Lon ATP-dependent Protease 1017 (CT859) lytB Metalloprotease 1009 (CT851) map Methionine Aminopeptidase 0385 (CT045) pepA Leucyl Aminopeptidase A 0136 (CT112) pepF Oligopeptidase 0813 (CT574) pepP Aminopeptidase P 0613 (CT494) sohB Protease 0555 (CT441) tsp Tail-Specific Protease 0344 (CT072) yaeL Metalloprotease 0981 (CT824) Zinc Metalloprotease (insulinase family) Protein Isomerases 0227 (CT176) dsbB Disulfide bond Oxidoreductase 0786 (CT595) dsbD Thio:disulfide Interchange Protein 0228 (CT177) dsbG Disulfide Bond Chaperone 0933 (CT783) Predicted Disulfide Bond Isomerase 0926 (CT780) Thioredoxin Disulfide Isomerase Transcription RNA Degradation 0999 (CT842) pnp Polyribonucleotide Nucleotidyltransferase 0054 (CT297) mc Ribonuclease III 0119 (CT029) mhB_1 Ribonuclease HII_1 1068 (CT008) mhB_2 Ribonuclease HII_2 0934 (CT784) mpA Ribonuclease P Protein Component 0504 (CT397) vacB Ribonuclease Family RNA Elongation & Termination Factors 0741 (CT636) greA Transcription Elongation Factor 0316 (CT097) nusA N Utilization Protein A 0076 (CT320) nusG Transcriptional Antitermination 0845 (CT704) pcnB_1 Poly A Polymerase_1 0966 (CT410) pcnB_2 Poly A Polymerase_2 0610 (CT491) rho Transcription Termination Factor RNA Methylases 0674 (CT553) fmu RNA Methyltransferase 1059 (CT354) kgsA Dimethyladenosine Transferase 0187 (CT133) Predicted Methylase 0530 (CT403) spoU_1 rRNA Methylase_1 0660 (CT540) spoU_2 rRNA Methylase_2 0117 (CT027) trmD tRNA (Guanine N-1)-Methyltransferase 0885 (CT742) ygcA rRNA Methyltransferase 0986 (CT829) yggH Predicted rRNA Methylase 0987 (CT830) ytgB Predicted rRNA Methylase RNA Modification 0649 (CT530) fmt Methionyl tRNA Formyltransferase 0910 (CT766) mizA tRNA Pyrophosphate Transferase 0719 (CT658) sfhB Predicted Pseudouridine Synthase 0219 (CT193) tgt Queuine tRNA Ribosyl Transferase 0580 (CT463) truA Pseudouridylate Synthase I 0319 (CT094)

truB tRNA Pseudouridine Synthase 0403 (CT106) yceC Predicted Pseudouridine Synthetase Family 0864 (CT723) yjbC Predicted Pseudouridine Synthase RNA Polymerase & Transcription Regulators 0586 (CT468) atpC Two-Component Regulator 0362 (CT061) rpsD Sigma-28/WhiG Family 0501 (CT394) hrcA HTH Transcriptional Repressor 0793 (CT588) rbsU Sigma Regulatory Family Protein-PP2C Phosphatase (RsbW Antagonist) 0626 (CT507) rpoA RNA Polymerase Alpha

US-PAT-NO: 6777536

DOCUMENT-IDENTIFIER: US 6777536 B1
See image for Certificate of Correction

TITLE: EPH receptor ligands, and uses related thereto

DATE-ISSUED: August 17, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Flanagan; John G.	Newton	MA	N/A	N/A
Cheng; Hwai-Jong	Boston	MA	N/A	N/A

APPL-NO: 08/ 393462

DATE FILED: February 27, 1995

PARENT-CASE:

REFERENCE TO RELATED APPLICATIONS

This application in a continuation-in-part of U.S. Ser. No. 08/308,814, filed Sep. 19, 1994, now abandoned, and entitled "EPH Receptor Ligands, and Uses Related Thereto". The disclosure of U.S. Ser. No. 08/308,814 is incorporated by reference.

US-CL-CURRENT: 530/350, 435/252.3 , 435/320.1 , 435/69.1 , 435/7.1 , 536/23.1 , 536/23.5

ABSTRACT:

The present invention relates to the discovery of a novel EPH receptor ligand, referred to hereinafter as "Elf-1", which protein has apparently broad involvement in the formation and maintenance of ordered spatial arrangements of differentiated tissues in vertebrates, and can be used to generate and/or maintain an array of different vertebrate tissue both in vitro and in vivo.

14 Claims, 13 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 12

---------- KWIC ---------

Detailed Description Text - DETX (69):
When it is desirable to express only a portion of an Elf-1 protein, such as a form lacking a portion of the N-terminus, i.e. a trunction mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-XX57) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722).

Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing Elf-1-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

US-PAT-NO: 6777217

DOCUMENT-IDENTIFIER: US 6777217 B1

TITLE: Histone deacetylases, and uses related thereto

DATE-ISSUED: August 17, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Schreiber; Stuart L.	Boston	MA	N/A	N/A
Taunton; Jack	Somerville	MA	N/A	N/A
Hassig; Christian A.	Somerville	MA	N/A	N/A
Jamison; Timothy F.	Cambridge	MA	N/A	N/A

APPL-NO: 08/ 624735

DATE FILED: March 26, 1996

US-CL-CURRENT: 435/194, 435/252.3 , 435/320.1 , 435/325 , 536/23.1 , 536/23.2

ABSTRACT:

The present invention concerns the discovery that proteins encoded by a family of genes, termed here HDx-related genes, which are involved in the control of chromatin structure and, thus in transcription and translation. The present invention makes available compositions and methods that can be utilized, for example to control cell proliferation and differentiation in vitro and in vivo.

11 Claims, 22 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 22

---------- KWIC --------

Detailed Description Text - DETX (72):

When it is desirable to express only a portion of an HDx protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing HDx-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

US-PAT-NO: 6767888

DOCUMENT-IDENTIFIER: US 6767888 B1

TITLE: Neuroprotective methods and reagents

DATE-ISSUED: July 27, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Mahanthappa; Nagesh K.	Cambridge	MA	N/A	N/A

APPL-NO: 09/ 418221

DATE FILED: October 14, 1999

PARENT-CASE:

This application is a continuation-in-part of U.S. patent application Ser. No. 08/883,656, filed Jun. 27, 1997, abandoned incorporated herein by reference in its entirety.

US-CL-CURRENT: 514/2, 436/501 , 514/279 , 514/309 , 514/312 , 530/350 , 536/23.1

ABSTRACT:

One aspect of the present application relates to a method for limiting damage to neuronal cells by ischemic or epoxic conditions, e.g., such as may be manifest by a reduction in brain infarct volume, by administering to an individual a hedgehog therapeutic or ptc therapeutic in an amount effective for reducing cerebral infarct volume.

8 Claims, 1 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 1

---------- KWIC ---------

Detailed Description Text - DETX (70):

When it is desirable to express only a portion of a hedgehog protein, such as a form lacking a portion of the N-terminus, i.e., a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al. (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al. (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing hedgehog-derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al., supra).

US-PAT-NO: 6747128

DOCUMENT-IDENTIFIER: US 6747128 B2

TITLE: Components of ubiquitin ligase complexes, and uses related thereto

DATE-ISSUED: June 8, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Caligiuri; Maureen	Reading	MA	N/A	N/A
Rolfe; Mark	Newton	MA	N/A	N/A

APPL-NO: 08/ 915048

DATE FILED: August 20, 1997

US-CL-CURRENT: 530/350, 435/183 , 435/219 , 435/252.3 , 435/254.11 , 435/320.1 , 435/325 , 536/23.1 , 536/23.2 , 536/23.5

ABSTRACT:

The present invention relates to the isolation of a new class of ubiquitin ligases involved in protein degradation in vertebrate organisms, such as protein degradation of cell cycle regulatory proteins. Accordingly, the invention provides nucleic acids and the proteins encoded by said nucleic acids which play a role in the ubiquitinylation and subsequent degradation of substrate proteins and in regulating cell proliferation, cell differentiation, and cell survival. The invention also provides methods for modulating protein degradation, cell proliferation, cell differentiation and/or cell survival by modulating protein ubiquitination; assays for identifying compounds which modulate protein degradation, cell proliferation, differentiation and/or cell survival; methods for treating disorders associated with aberrant protein degradation, cell proliferation, cell differentiation, and/or cell survival; and diagnostic and prognostic assays for determining whether a subject is at risk of developing a disorder associated with an aberrant protein degradation, cell proliferation, cell differentiation, and/or survival.

18 Claims, 0 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 2

---------- KWIC ---------

Detailed Description Text - DETX (111):

When expression of a carboxy terminal fragment of the full-length SIP proteins is desired, i.e. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat et al., (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its in vitro activity has been demonstrated on recombinant proteins (Miller et al.,

(1987) PNAS USA 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either in vivo by expressing such recombinant polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or in vitro by use of purified MAP (e.g., procedure of Miller et al.).

US-PAT-NO: 6730303

DOCUMENT-IDENTIFIER: US 6730303 B1

TITLE: Fused G-CSF and IL-3 proteins and uses thereof

DATE-ISSUED: May 4, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Feng; Yiqing	St. Louis	MO	N/A	N/A
Staten; Nicholas R.	St. Louis	MO	N/A	N/A
Baum; Charles M.	Evanston	IL	N/A	N/A
Summers; Neena L.	St. Charles	MO	N/A	N/A
Caparon; Maire Helena	Chesterfield	MO	N/A	N/A
Bauer; S. Christopher	New Haven	MO	N/A	N/A
Zurfluh; Linda L.	Kirkwood	MO	N/A	N/A
McKearn; John P.	Glencoe	MO	N/A	N/A
Klein; Barbara K.	St. Louis	MO	N/A	N/A
Lee; Stephen C.	St. Louis	MO	N/A	N/A
McWherter; Charles A.	Wildwood	MO	N/A	N/A
Giri; Judith G.	Chesterfield	MO	N/A	N/A

APPL-NO: 09/ 510238

DATE FILED: February 22, 2000

PARENT-CASE:

The present application is a divisional of U.S. Ser. No. 08/835,162 filed Apr. 4, 1997 and issued as U.S. Pat. No. 6,066,318 which is a Continuation-in-Part of U.S. Ser. No. 08/836,659 which was filed as PCT/US 96/15774 on Oct. 4, 1996 which claims priority under 35 USC .sctn.119(e) of U.S. provisional application Ser. No. 60/004,834 filed Oct. 5, 1995.

The present application is a Continuation-in-Part of PCT/US 96/15774 filed Oct. 4, 1996 which claims priority under 35 USC .sctn.119(e) of U.S. provisional application Ser. No. 60/004,834 filed Oct. 5, 1995.

US-CL-CURRENT: 424/192.1, 424/198.1 , 424/85.1 , 424/85.2 , 424/93.21 , 435/252.3 , 435/320.1 , 435/372 , 435/69.7 , 435/69.9 , 530/351 , 530/399 , 536/23.4

ABSTRACT:

Disclosed are novel multi-functional hematopoietic receptor agonist proteins, DNAs which encode the multi-functional hematopoietic receptor agonists proteins, methods of making the multi-functional hematopoietic receptor agonists proteins and methods of using the multi-functional hematopoietic receptor agonists proteins.

27 Claims, 4 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 4

---------- KWIC --------

Detailed Description Text - DETX (41):

As another aspect of the present invention, there is provided a method for producing the novel multi-functional hematopoietic receptor agonists. The method of the present invention involves culturing suitable cells or cell line, which has been transformed with a vector containing a DNA sequence coding for expression of a novel multi-functional hematopoietic receptor agonist. Suitable cells or cell lines may be bacterial cells. For example, the various strains of E. coli are well-known as host cells in the field of biotechnology. Examples of such strains include E. coli strains JM101 (Yanish-Perron et al. Gene 33: 103-119, 1985) and MON105 (Obukowicz et al., Applied Environmental Microbiology 58: 1511-1523, 1992). Also included in the present invention is the expression of the multi-functional hematopoietic receptor agonist protein utilizing a chromosomal expression vector for E. coli based on the bacteriophage Mu (Weinberg et al., Gene 126: 25-33, 1993). Various strains of B. subtilis may also be employed in this method. Many strains of yeast cells known to those skilled in the art are also available as host cells for expression of the polypeptides of the present invention. When expressed in the E. coli cytoplasm, the gene encoding the multi-functional hematopoietic receptor agonists of the present invention may also be constructed such that at the 5' end of the gene codons are added to encode Met.sup.-2 -Ala.sup.-1 - or Met.sup.-1 at the N-terminus of the protein. The N termini of proteins made in the cytoplasm of E. coli are affected by post-translational processing by methionine aminopeptidase (Ben Bassat et al., J. Bac. 169:751-757, 1987) and possibly by other peptidases so that upon expression the methionine is cleaved off the N-terminus. The multi-functional hematopoietic receptor agonists of the present invention may include multi-functional hematopoietic receptor agonist polypeptides having Met.sup.-1, Ala.sup.-1 or Met.sup.-2 -Ala.sup.-1 at the N-terminus. These mutant multi-functional hematopoietic receptor agonists may also be expressed in E. coli by fusing a secretion signal peptide to the N-terminus. This signal peptide is cleaved from the polypeptide as part of the secretion process.

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	559	methionine adj aminopeptidase$	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:01
L2	8602	(methionine or met) same muta$10	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02
L3	223	1 same 2	US-PGPUB; USPAT	OR	OFF	2005/03/24 14:02
L4	2380	methionine same cysteine same muta$10	US-PGPUB; USPAT	OR	OFF	2005/03/24 15:59
L5	121	4 same stab$8	US-PGPUB; USPAT	OR	OFF	2005/03/24 16:00

PGPUB-DOCUMENT-NUMBER: 20050064526

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050064526 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: March 24, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ulrich, Robert G.	Frederick	MD	US	
Olson, Mark A.	Gaithersburg	MD	US	
Bavari, Sina	Dillsburg	PA	US	

APPL-NO: 10/ 767687

DATE FILED: January 29, 2004

RELATED-US-APPL-DATA:

child 10767687 A1 20040129

parent division-of 08882431 19970625 US GRANTED

parent-patent 6713284 US

US-CL-CURRENT: 435/7.32, 424/190.1 , 435/252.3 , 435/320.1 , 435/69.1 , 530/395 , 536/23.7

ABSTRACT:

The present invention relates to genetically attenuated superantigen toxin vaccines altered such that superantigen attributes are absent, however the superantigen is effectively recognized and an appropriate immune response is produced. The attenuated superantigen toxins are shown to protect animals against challenge with wild type toxin. Methods of producing and using the altered superantigen toxins are described.

---------- KWIC ---------

Detail Description Paragraph - DETX (9):

[0047] The binding interface between SEB and HLA-DR1 consists principally of two structurally conserved surfaces located in the N-terminal domain: a polar binding pocket derived from three .beta.-strand elements of the .beta.-barrel domain and a hydrophobic reverse turn. The binding pocket of SEB contains residues E67 (E=Glutamic acid), Y89 (Y=Tyrosine) and Y115 (Y=tyrosine), and binds K39 (K=Lysine) of the DR.alpha. subunit. The amino acid one letter code is defined as the following: A=Alanine (Ala), I=Isoleucine (Ile), L=Leucine (Leu), M=Methionine (Met), F=Phenylalanine (Phe), P=Proline (Pro), W=Tryptophan (Trp), V=Valine (Val), N=Asparagine (Asn), C=Cysteine (Cys), Q=Glutamine (Q), G=Glycine (Gly), S=Serine (Ser), T=Threonine (Thr), Y=Tyrosine (Tyr), R=Arginine (Arg), H=Histidine (His), K=Lysine (Lys), D=Aspartic acid (Asp), and E=Glutamic acid (Glu). For SEA, the binding interface with the DR molecule is modeled to contain a similar binding pocket consisting of residues D70, Y92 and Y108. Mutation of residue Y89 in SEB or Y92 in SEA to alanine (FIG. 2)

resulted in greater than 100-fold reduction in DR1 binding. The substitution of alanine for Y89 in SEB and Y92 in SEA eliminates the hydrogen bond with K39 and disrupts packing interactions with adjacent protein residues. Modeling of the SEA mutant Y92A predicts an increase in solvent-accessible surface area for Y108 by a factor of two greater than the wild-type structure, allowing the formation of a hydrogen bond to the carboxylate group of D70 and thus disrupting key anchoring and recognition points for HLA-DR1. This effect is expected to be somewhat less in SEB due to the longer side chain at E67. Substitution of SEB Y115 with alanine also resulted in greater than 100-fold reduction of binding. In contrast, the same replacement of Y108 in SEA yielded little to no change in DR1 binding (FIG. 2a), suggesting the primary importance of SEA residues Y92 and D70 for stabilizing interactions with K39. The K39 side chain of DR.alpha. forms a strong ion-pair interaction with the SEB E67 carboxylate group and hydrogen bonds with the hydroxyl groups of Y89 and Y115. Substitution of SEB E67 by glutamine reduced binding affinity by greater than 100-fold (FIG. 2), reflecting the replacement of the strong ionic bond with a weaker hydrogen bond. To optimize ion-pair interactions of the analogous SEA site, the shorter carboxylate side chain of D70 is predicted to shift K39 of DR.alpha., weakening interactions with SEA Y108. The substitution of alanine for SEA Y108 is thus more easily accommodated than the homologous substitution of SEB Y115, without loss in DR1 binding.

PGPUB-DOCUMENT-NUMBER: 20050048527

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050048527 A1

TITLE: Endonuclease-substrate complexes

PUBLICATION-DATE: March 3, 2005

INVENTOR-INFORMATION:

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APPL-NO: 10/ 783557

DATE FILED: February 20, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60448601 20030220 US

non-provisional-of-provisional 60452008 20030304 US

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US01/44953	2001WO-PCT/US01/44953	November 15, 2001

US-CL-CURRENT: 435/6

ABSTRACT:

The present invention provides novel cleavage agents for the cleavage and modification of nucleic acid. The cleavage agents find use, for example, for the detection and characterization of nucleic acid sequences and variations in nucleic acid sequences. In some embodiments, an endonuclease activity is used to cleave a target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof.

[0001] The present application claims priority to U.S. Provisional Application Ser. No. 60/448, 601, filed Feb. 20, 2003, and U.S. Provisional Application Ser. No. 60/452,008, filed Mar. 4, 2003, each of which is incorporated herein by reference. The present application also incorporates by reference co-pending U.S. patent application Ser. No. 09/714,935, filed Nov. 17, 2000, U.S. patent application Ser. No. 10/290,386, filed Nov. 11, 2002, and PCT Application No. PCT/US01/44953, filed Nov. 15, 2001, each in their entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (256):
[0623] Some embodiments of the present invention provide mutant or variant

forms of enzymes described herein. It is possible to modify the structure of a peptide having an activity of the enzymes described herein for such purposes as enhancing cleavage rate, substrate specificity, stability, and the like. For example, a modified peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition. For example, it is contemplated that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e., conservative mutations) will not have a major effect on the biological activity of the resulting molecule. Accordingly, some embodiments of the present invention provide variants of enzymes described herein containing conservative replacements. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine); (3) nonpolar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); and (4) uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar fashion, the amino acid repertoire can be grouped as (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine histidine), (3) aliphatic (glycine, alanine, valine, leucine, isoleucine, serine, threonine), with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic (phenylalanine, tyrosine, tryptophan); (5) amide (asparagine, glutamine); and (6) sulfur-containing (cysteine and methionine) (See e.g., Stryer (ed.), Biochemistry, 2nd ed, WH Freeman and Co. [1981]). Whether a change in the amino acid sequence of a peptide results in a functional homolog can be readily determined by assessing the ability of the variant peptide to produce a response in a fashion similar to the wild-type protein using the assays described herein. Peptides in which more than one replacement has taken place can readily be tested in the same manner.

PGPUB-DOCUMENT-NUMBER: 20050037053

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050037053 A1

TITLE: Animal feed

PUBLICATION-DATE: February 17, 2005

INVENTOR-INFORMATION:

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APPL-NO: 10/ 497315

DATE FILED: October 6, 2004

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
GB	0129864.5	2001GB-0129864.5	December 13, 2001

PCT-DATA:
APPL-NO: PCT/IB02/05771
DATE-FILED: Dec 13, 2002
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 424/442, 426/53 , 426/54

ABSTRACT:

The present invention relates to a component comprising an enzyme for use in a feed comprising strach: wherein the enzyme has amylase activity and is capable of degrading resistant starch.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (87):
[0077] In order to alter the stability or activity profile of amylase enzymes under varying conditions, it has been found that selective replacement, substitution or deletion of oxidizable amino acids, such as a methionine, tryptophan, tyrosine, histidine or cysteine, results in an altered profile of the variant enzyme as compared to its precursor. Because currently commercially available amylases are not acceptable (stable) under various conditions, there is a need for an amylase having an altered stability and/or activity profile. This altered stability (oxidative, thermal or pH performance profile) can be achieved while maintaining adequate enzymatic activity, as compared to the wild-type or precursor enzyme. The characteristic affected by introducing such mutations may be a change in oxidative stability while maintaining thermal stability or vice versa. Additionally, the substitution of different amino acids for an oxidizable amino acids in the alpha-amylase

precursor sequence or the deletion of one or more oxidizable amino acid(s) may result in altered enzymatic activity at a pH other than that which is considered optimal for the precursor alpha-amylase. In other words, the mutant enzymes of the present invention may also have altered pH performance profiles, which may be due to the enhanced oxidative stability of the enzyme.

PGPUB-DOCUMENT-NUMBER: 20050005323

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050005323 A1

TITLE: Method for increasing product yield

PUBLICATION-DATE: January 6, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Birch, Robert George	Jindalee		AU	
Wu, Luguang	Kenmore		AU	

APPL-NO: 10/ 845059

DATE FILED: May 12, 2004

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
AU	2003902253	2003AU-2003902253	May 12, 2003

US-CL-CURRENT: 800/278, 435/162 , 435/419 , 435/468 , 800/284 , 800/287

ABSTRACT:

The present invention relates to methods for increasing the yield of a compound produced by an organism. More particularly, the present invention relates to methods for increasing the total or soluble carbohydrate content or sweetness or increasing the content of an endogenous carbohydrate of a plant tissue by producing a sugar-metabolizing enzyme that catalyzes the conversion of an endogenous sugar (one that is normally produced in the plant) to an alien sugar (one that is not normally produced in the plant at the same developmental stage). The invention also relates to plants and plant parts that produce a sugar-metabolizing enzyme to yield an alien sugar, with the consequence of higher total fermentable carbohydrate content, and to fermentable carbohydrates and other products derived therefrom.

---------- KWIC ---------

Detail Description Paragraph - DETX (52):

[0110] In another embodiment, the level of conversion of the endogenous sugar to the alien sugar is modulated by using sugar-metabolizing enzymes of different functional activities. This may arise from differences in the specific activities or **stabilities** of the enzymes in the cellular compartment where the sugar conversion is accomplished. In certain embodiments, the activity of a sugar-metabolizing enzyme that is used for the conversion of the endogenous sugar to the alien sugar is at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90%, or even at least about 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000% higher, or at least about 10%, 20%, 30% 40%, 50%, 60%, 70%, 80%, 90%, 92%, 94%, 96%, 97%, 98% or 99%, or even at least about 99.5%, 99.9%, 99.95%, 99.99%, 99.995% or 99.999% lower than that of a reference enzyme. Sugar-metabolizing enzymes of different activities may be naturally occurring or may be obtained by synthetic or recombinant means, for example, by modification of the catalytic site or any other site (e.g., substrate-binding site, co-factor binding site) of a reference or parent enzyme. Typically, the

modification is achieved by the substitution, addition or deletion of at least one amino acid in the sequence of parent enzyme using for example rational or established methods of mutagenesis or combinatorial chemistries, as are known in the art. Variant sugar-metabolizing enzymes may comprise conservative amino acid substitutions. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, an amino acid residue in a parent enzyme is suitably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a polynucleotide that codes for the reference enzyme, such as by saturation mutagenesis, and the resultant mutants can be screened for enzyme activity to identify mutants with a different activity than the parent enzyme. The enzymes of interest may be tested for relative activity for example using the method in Example 2, modified by incubation of the crude or purified enzyme preparations before and/or during the assay in conditions resembling the plant cellular compartment where the sugar conversion is to be accomplished, as an additional test of stability and specific activity under these conditions.

PGPUB-DOCUMENT-NUMBER: 20040248231

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040248231 A1

TITLE: Modulation of Abeta levels by beta-secretase BACE2

PUBLICATION-DATE: December 9, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 10/ 749714

DATE FILED: December 31, 2003

RELATED-US-APPL-DATA:

child 10749714 A1 20031231

parent division-of 09886143 20010620 US GRANTED

parent-patent 6713276 US

non-provisional-of-provisional 60215729 20000628 US

US-CL-CURRENT: 435/23

ABSTRACT:

The present invention is based on the findings that BACE2, a homolog of .beta.-secretase BACE, is able to stimulate processing of APP in a non-amyloidogenic pathway, thereby suppressing the level of A.beta.. Accordingly, the present invention provides methods and means for the identification and use of modulators of this unique activity of BACE2 to suppress A.beta. production. The compounds identified using the methods and means provided herein may be used as potential candidates for the treatment of Alzheimer's disease and other neurological diseases.

[0001] This application claims priority under 35 U.S.C. .sctn.119(e) to U.S. Provisional Application No. 60/215,729 filed Jun. 28, 2000.

---------- KWIC ---------

Detail Description Paragraph - DETX (125):

[0144] As described above, BACE2 expression resulted in the accumulation of APP CTFs concomitant with the reduction of A.beta. levels. This effect prompted investigation into whether .beta.-secretase cleavage was required for A.beta. suppression. The effects of BACE2 on the metabolism of the C-terminal 100 amino acids of APP (CT100), a construct that mimics prior .beta.-secretase

cleavage (Shoji et al., Science 258: 126-129 [1992]), was analyzed. When CT100 was expressed in HEK293T cells, A.beta. levels were significantly increased over mock-transfected cells (FIG. 5A). As expected, additional BACE copies did not affect the levels of A.beta. under CT100 overexpression conditions. Co-expression of BACE2 and CT100 resulted in the dramatic suppression of total A.beta. as well as A.beta.42 levels (FIG. 5a, b). Thus, the capacity of BACE2 to suppress A.beta. formation does not require prior .beta.-secretase cleavage. The dramatic reduction in A.beta. formation was confirmed by Western blotting of conditioned medium and the CTFs in the lysate (FIG. 5c). BACE2 also led to the accumulation of a fragment that corresponded in size to .alpha.-CTF. At steady-state, this was accompanied by a partial reduction in CT100 which corresponds to .beta.-CTF confirming that .beta.-CTF could be converted to .alpha.-CTF under these BACE2 conditions. To confirm that there was a precursor-product relationship between .beta.-CTF (i.e., CT100) and the .alpha.-like CTF that accumulated upon BACE2 overexpression, a pulse-chase analysis was performed. HEK293 cells were transfected with CT100 alone or CT100 with BACE2. Cells were readiolabeled with .sup.35S-methionine/cysteine for 15 minutes after which the medium containing radiolabel was removed and replaced with standard medium. The cells were then incubated for 90 minutes. Over this 90-minute period, samples were taken and assessed for CTFs by immunoprecipitation. Under these CT100 transfection conditions, endogenous APP was negligible in the formation of CTFs. While CT100 was fairly stable in mock-transfected cells, BACE2 expression yielded a pattern of CTFs that was identical to that observed when APP was co-transfected (FIG. 5d). Again, BACE2 resulted in the accumulation of the .alpha.-like CTF, clearly indicating that it was derived from CT100. This effect was rescued when a critical aspartate residue was mutated in BACE2 (D110A in FIG. 5d; also see below). This indicates that BACE2 has .alpha.-secretase-like activity. Taken together, these data indicate that the ability of BACE2 to suppress A.beta. production reflects enhanced .alpha.-secretase-like activity that is independent of prior .beta.-secretase cleavage. This .alpha.-secretase-like activity of BACE2 promotes the non-amyloidogenic processing of APP or APP fragments and reduces the production of A.beta..

PGPUB-DOCUMENT-NUMBER: 20040214174

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040214174 A1

TITLE: Reactions on a solid surface

PUBLICATION-DATE: October 28, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 10/ 309584

DATE FILED: December 4, 2002

RELATED-US-APPL-DATA:

child 10309584 A1 20021204

parent continuation-in-part-of 09732622 20001208 US PENDING

child 09732622 20001208 US

parent continuation-in-part-of 09350309 19990709 US GRANTED

parent-patent 6348314 US

child 09350309 19990709 US

parent division-of 08756386 19961126 US GRANTED

parent-patent 5985557 US

child 09732622

parent continuation-in-part-of 09381212 20000208 US PENDING

child 09381212 20000208 US

parent a-371-of-international PCT/US98/05809 19980324 WO PENDING

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US97/01072	1997WO-PCT/US97/01072	January 22, 1997

US-CL-CURRENT: 435/6, 435/287.2

ABSTRACT:

The present invention relates to compositions and methods for the detection and characterization of nucleic acid sequences and variations in nucleic acid sequences. The present invention relates to methods for forming a nucleic acid

cleavage structure on a solid support and cleaving the nucleic acid cleavage structure in a site-specific manner. For example, in some embodiments, a 5' nuclease activity from any of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof.

[0001] The present invention is a continuation-in-part of co-pending U.S. application Ser. No. 09/732,622, which is a continuation-in-part of co-pending U.S. application Ser. No. 09/350,309, which is a divisional application of U.S. Pat. No. 5,985,557; is also a continuation-in-part of co-pending U.S. application Ser. No. 09/381,212, which is a national entry of PCT Appl. No. US 98/05809, which claims priority to U.S. Pat. Nos. 5,994,069, 6,090,543, 5,985,557, 6,001,567, and 5,846,717 and PCT Appln. No. US 97/01072; each of which is incorporated by reference herein in its entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (247):

[0616] Some embodiments of the present invention provide mutant or variant forms of enzymes described herein. It is possible to modify the structure of a peptide having an activity of the enzymes described herein for such purposes as enhancing cleavage rate, substrate specificity, stability, and the like. For example, a modified peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition. For example, it is contemplated that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e., conservative mutations) will not have a major effect on the biological activity of the resulting molecule. Accordingly, some embodiments of the present invention provide variants of enzymes described herein containing conservative replacements. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine); (3) nonpolar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); and (4) uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar fashion, the amino acid repertoire can be grouped as (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine histidine), (3) aliphatic (glycine, alanine, valine, leucine, isoleucine, serine, threonine), with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic (phenylalanine, tyrosine, tryptophan); (5) amide (asparagine, glutamine); and (6) sulfur-containing (cysteine and methionine) (See e.g., Stryer (ed.), Biochemistry, 2nd ed, WH Freeman and Co. [1981]). Whether a change in the amino acid sequence of a peptide results in a functional homolog can be readily determined by assessing the ability of the variant peptide to produce a response in a fashion similar to the wild-type protein using the assays described herein. Peptides in which more than one replacement has taken place can readily be tested in the same manner.

PGPUB-DOCUMENT-NUMBER: 20040209817

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040209817 A1

TITLE: Methods and compositions for the treatment of peripheral artery disease

PUBLICATION-DATE: October 21, 2004

INVENTOR-INFORMATION:

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APPL-NO: 10/ 845911

DATE FILED: May 14, 2004

RELATED-US-APPL-DATA:

child 10845911 A1 20040514

parent continuation-of 09886856 20010621 US ABANDONED

non-provisional-of-provisional 60213504 20000622 US

non-provisional-of-provisional 60264572 20010126 US

non-provisional-of-provisional 60276549 20010316 US

US-CL-CURRENT: 514/12

ABSTRACT:

Compositions and methods for treating peripheral artery disease in a patient are provided. Compositions comprise recombinant fibroblast growth factor-2. Fibroblast growth factor, such as FGF-2, is administered in therapeutically effective amounts to treat or prevent peripheral artery disease including claudication and critical limb ischemia. Pharmaceutical compositions comprising a therapeutically effective amount of FGF-2 and a pharmaceutically acceptable carrier are also provided. The methods of the invention to treat peripheral artery disease and claudication comprise administering at least a single dose of a pharmaceutical composition comprising the FGF, such as FGF-2, via intra-arterial, intravenous, or intramuscular infusion to the patient. It is recognized that increased benefits may result from multiple dosing, including intermittent dosing.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. application Ser. No. 09/886,856; filed Jun. 21, 2001, which claims the benefit of U.S. Provisional Application Serial Nos. 60/213,504, filed Jun. 22, 2000, 60/264,572, filed Jan. 26, 2001, and 60/276,549, filed Mar. 16, 2001, each of which is entitled "Methods and Compositions for the Treatment of Peripheral Artery Disease," the contents of which are herein incorporated by reference in their entirety.

---------- KWIC --------

Detail Description Paragraph - DETX (46):

[0073] The unit dose of the present invention also comprises an "angiogenically active mutein" of the FGF-2 of FIG. 2 (SEQ ID NO:2), FIG. 3 (SEQ ID NO:4), FIG. 4 (SEQ ID NO:6), or FIG. 5 (SEQ ID NO:8). By the term "angiogenically active mutein" is intended a mutated form of the FGF-2 of FIG. 2 (SEQ ID NO:2), FIG. 3 (SEQ ID NO:4), FIG. 4 (SEQ ID NO:6), or FIG. 5 (SEQ ID NO:8) that structurally retains at least 80%, preferably 90%, of the 146 residues of the FGF-2 sequence shown in FIG. 2 (SEQ ID NO: 2), the 146 residues of the human FGF-2 sequence shown in FIG. 3 (SEQ ID NO:4), the 155 residues of the FGF-2 sequence shown in FIG. 4 (SEQ ID NO:6), or the 155 residues of the FGF-2 sequences shown in FIG. 5 (SEQ ID NO:8), respectively, in their respective positions, and that functionally retains the angiogenic activity of the respective unmutated form of FGF-2. Preferably, the mutations are "conservative substitutions" using L-amino acids, wherein one amino acid is replaced by another biologically similar amino acid. Examples of conservative substitutions include the substitution of one hydrophobic residue such as Ile, Val, Leu, Pro, or Gly for another, or the substitution of one polar residue for another, such as between Arg and Lys, between Glu and Asp, or between Gln and Asn, and the like. Generally, the charged amino acids are considered interchangeable with one another. However, to make the substitution more conservative, one takes into account both the size and the likeness of the charge, if any, on the side chain. Suitable substitutions include the substitution of serine for one or both of the cysteines at residue positions 87 and 92, which are not involved in disulfide formation. Other suitable substitutions include any substitution wherein at least one constituent cysteine is replaced by another amino acid so that the mutein has greater stability under acidic conditions, see for example U.S. Pat. No. 5,852,177 which is herein incorporated by reference. One such substitution is the replacement of cysteine residues with neutral amino acids such as for example: glycine, valine, alanine, leucine, isoleucine, tyrosine, phenylalanine, histidine, tryptophan, serine, threonine, and methionine (U.S. Pat. No. 5,852,177). Preferably, substitutions are introduced at the FGF-2 N-terminus, which is not associated with angiogenic activity. However, as discussed above, conservative substitutions are suitable for introduction throughout the molecule.

PGPUB-DOCUMENT-NUMBER: 20040191265

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040191265 A1

TITLE: Stabilized glycoproteins

PUBLICATION-DATE: September 30, 2004

INVENTOR-INFORMATION:

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Feng, Jinhua	North Potomac	MD	US	
Tous, Guillermo	Gaithersburg	MD	US	

APPL-NO: 10/ 751744

DATE FILED: January 5, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60438162 20030106 US

US-CL-CURRENT: 424/184.1

ABSTRACT:

The present invention provides stabilized immunoglobulin molecules that have increased storage stability and/or in vivo half-lives due to the mutation of one or more amino acids that would otherwise render the immunoglobulin molecules susceptible to degradation. In a preferred embodiment, the stabilized immunoglobulins of the invention have mutations at the heavy chain constant domain hinge region. Such stabilized immunoglobulin molecules, i.e., immunoglobulin molecules with increased storage stability have one or more of the following advantages they are more readily transported and/storable for longer periods and/or less stringent conditions than non-stabilized counterparts; that smaller amounts and or less frequent dosing is required in the therapeutic, prophylactic or diagnostic use of such stabilized molecules.

[0001] This application is entitled to the benefit and claims priority under 35 U.S.C. .sctn. 119(e) to U.S. Provisional Application Serial No. 60/438,162, filed Jan. 6, 2003, which is incorporated herein by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (51):

[0089] The stabilized immunoglobulins of the invention may comprise, in addition or in place of one or more modifications at the heavy chain hinge regions, one or more modifications in sequences flanking the heavy chain hinge regions, for example the CH1 or CH2 domains. For example, stabilized immunoglobulin of the present invention can have one or more stabilizing mutations in the CH2 domain immediately C terminal to the hinge region. In a preferred embodiment, the stabilized immunoglobulin has one or more stabilizing

mutations in one or more of the following amino acids: L(247)L(248)G(249)G(250)P(251) of human IgG1 or corresponding residues in other immunoglobulins. In a specific preferred embodiment, the mutation is at IgG1 position 249. In a specific embodiment, the glycine at position 249 of IgG1 is substituted with alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine.

Detail Description Table CWU - DETL (2):

2TABLE 6 Exemplary heavy chain hinge region stabilizing mutations. Heavy chain hinge region position Stabilizing point mutation(s) Cysteine 233 and/or Alanine, arginine, asparagine, aspartic acid, glutamic acid, cysteine 239 (human gamma 1) glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine Aspartic Acid 234 (human gamma 1) Alanine, arginine, asparagine, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine Lysine 235 (human gamma 1) Alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine Threonine 236 and/or Alanine, arginine, asparagine, aspartic acid, cysteine, glutamic threonine 239 (human gamma 1) acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, tryptophan, tyrosine, valine Histidine 237 (human gamma 1) Alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine Serine 236 (human gamma 4) Proline

PGPUB-DOCUMENT-NUMBER: 20040161821

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040161821 A1

TITLE: DEP-1 receptor protein tyrosine phosphatase interacting proteins and related methods

PUBLICATION-DATE: August 19, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Palka-Hamblin, Helena L.	Rego Park	NY	US	
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APPL-NO: 10/ 723606

DATE FILED: November 26, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60429746 20021126 US

US-CL-CURRENT: 435/69.1

ABSTRACT:

Proteins are identified from human breast tumor cell lines (MDA-MB-231, T-47D and T-47D/Met) that interact specifically with the substrate-trapping mutant form of Density Enhanced Phosphatase-1 (DEP-1). These proteins include the functional component p120 catenin (p120.sup.ctn), the adaptor protein Gab 1, and the HGF/SF receptor Met. The invention relates to isolated complexes comprising DEP-1 polypeptides in specific association with Met, Gab 1, or p120.sup.ctn, identified herein as DEP-1 substrate polypeptides. Screening assays for agents that alter DEP-1 interaction with DEP-1 substrate polypeptides are also disclosed, as are methods for altering biological signals in cells that are transduced via DEP-1 pathways.

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 60/429,746 filed Nov. 26, 2002, which is incorporated herein by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (34):

[0066] Although the specific examples of mutant DEP-1 polypeptides described herein are DA (aspartate to alanine) mutants, YF (tyrosine to phenylalanine) mutants, CS mutants and combinations thereof, it will be understood that the subject invention substrate trapping mutant DEP-1 polypeptides are not limited to these amino acid substitutions. The invariant aspartate residue can be changed, for example by site-directed mutagenesis, to any amino acid that does not cause significant alteration of the Km of the enzyme but which results in a reduction in Kcat to less than 1 per minute (less than 1 min.sup.-). For example, the invariant aspartate residue can be changed or mutated to an

alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophan, methionine, glycine, serine, threonine, cysteine, tyrosine, asparagine, glutamine, lysine, arginine or histidine, or other natural or non-natural amino acids known in the art including derivatives, variants and the like. Similarly, substitution of at least one tyrosine residue may be with any amino acid that is not capable of being phosphorylated (i.e., stable, covalent modification of an amino acid side chain at a hydroxyl with a phosphate group), for example alanine, cysteine, aspartic acid, glutamine, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, asparagine, proline, arginine, valine or tryptophan, or other natural or non-natural amino acids known in the art including derivatives, variants and the like.

PGPUB-DOCUMENT-NUMBER: 20040141946

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040141946 A1

TITLE: Methods of treating neurological conditions with hematopoietic growth factors

PUBLICATION-DATE: July 22, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Schaebitz, Wolf-Ruediger	Dossenheim		DE	
Schneider, Armin	Heidelberg		DE	
Krueger, Carola	Speyer		DE	
Sommer, Clemens	Guenzburg		DE	
Schwab, Stefan	Heidelberg		DE	
Kollmar, Rainer	Heidelberg		DE	
Maurer, Martin	Heidelberg		DE	
Weber, Daniela	Mannheim		DE	
Gassler, Nikolaus	Heidelberg		DE	

APPL-NO: 10/ 659295

DATE FILED: September 11, 2003

RELATED-US-APPL-DATA:

child 10659295 A1 20030911

parent continuation-of 10331755 20021231 US PENDING

US-CL-CURRENT: 424/85.1, 424/85.2 , 514/12

ABSTRACT:

The present invention relates to a method of treating neurological conditions in a mammal by administering a hematopoietic growth factor such as granulocyte-colony stimulating factor (GCSF) and granulocyte-macrophage colony stimulating factor (GMCSF). The invention also provides methods of screening for compounds that bind to a GCSF or GMCSF receptor found on the surface of a neuronal cell; and which provides a neuroprotective, neuroproliferative and/or a STAT gene activation activity.

---------- KWIC --------

Detail Description Paragraph - DETX (7):

[0057] Additional examples of GCSF derivatives include a fusion protein of albumin and GCSF (Albugranin.TM.), or other fusion modifications such as those disclosed in U.S. Pat. No. 6,261,250); PEG-GCSF conjugates; those described in WO 00/44785 and Viens et al., J of Clin. Oncology, V1., Nr. 1, 2002: 24-36; norleucine analogues of GCSF, those described in U.S. Pat. No. 5,599,690; GCSF mimetics, such as those described in WO 99/61445, WO 99/61446, and Tian et al., Science, Vol. 281, 1998:257-259; GCSF muteins, where single or multiple amino acids have been modified, deleted or inserted, as described in U.S. Pat. Nos. 5,214,132 and 5,218,092; those GCSF derivatives described in U.S. Pat.

No. 6,261,550 and U.S. Pat. No. 4,810,643; and chimeric molecules, which contain the full sequence or a portion of GCSF in combination with other sequence fragments, e.g. Leridistim--see, for example, Streeter, et al. (2001) Exp. Hematol., 29, 41-50, Monahan, et al. (2001) Exp. Hematol., 29, 416-24., Hood, et al. (2001) Biochemistry, 40, 13598-606, Farese et al. (2001) Stem Cells, 19, 514-21, Farese, et al. (2001) Stem Cells, 19, 522-33, MacVittie, et al. (2000) Blood, 95, 837-45. Additionally, the GCSF derivatives include those with the cysteines at positions 17, 36, 42, 64, and 74 (of the 174 amino acid species (SEQ ID NO:37) or of those having 175 amino acids, the additional amino acid being an N-terminal methionine (SEQ ID NO:38)) substituted with another amino acid, (such as serine) as described in U.S. Pat. No. 6,004,548, GCSF with an alanine in the first (N-terminal) position; the modification of at least one amino group in a polypeptide having GCSF activity as described in EP 0 335 423; GCSF derivatives having an amino acid substituted or deleted in the N-terminal region of the protein as described in EP 0 272 703; derivatives of naturally occurring GCSF having at least one of the biological properties of naturally occurring GCSF and a solution stability of at least 35% at 5 mg/ml in which the derivative has at least Cys.sup.17 of the native sequence replaced by a Ser.sup.17 residue and Asp.sup.27 of the native sequence replaced by a Ser.sup.27 residue as described in EP 0 459 630; a modified DNA sequence encoding GCSF where the N-terminus is modified for enhanced expression of protein in recombinant host cells, without changing the amino acid sequence of the protein as described in EP 0 459 630; a GCSF which is modified by inactivating at least one yeast KEX2 protease processing site for increased yield in recombinant production using yeast as described in EP 0 243 153; lysine altered proteins as described in U.S. Pat. No. 4,904,584; cysteine altered variants of proteins as described in WO/9012874 (U.S. Pat. No. 5,166,322); the addition of amino acids to either terminus of a GCSF molecule for the purpose of aiding in the folding of the molecule after prokaryotic expression as described in AU-A-10948/92; substituting the sequence Leu-Gly-His-Ser-Leu-Gly-Ile (SEQ ID NO:11) at position 50-56 of GCSF with 174 amino acids (SEQ ID NO:37), and position 53 to 59 of the GCSF with 177 amino acids (SEQ ID NO:39), or/and at least one of the four histadine residues at positions 43, 79, 156 and 170 of the mature GCSF with 174 amino acids (SEQ ID NO:37) or at positions 46, 82, 159, or 173 of the mature GCSF with 177 amino acids (SEQ ID NO:39) as described in AU-A-76380/91; and a synthetic GCSF-encoding nucleic acid sequence incorporating restriction sites to facilitate the cassette mutagenesis of selected regions and flanking restriction sites to facilitate the incorporation of the gene into a desired expression system as described in GB 2 213 821.

PGPUB-DOCUMENT-NUMBER: 20040126754

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040126754 A1

TITLE: Multi-mer peptides derived from hepatitis C virus envelope proteins for diagnostic use and vaccination purposes

PUBLICATION-DATE: July 1, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Maertens, Geert	Brugge		BE	
Depla, Erik	Dealalbergen		BE	

APPL-NO: 10/ 685435

DATE FILED: October 16, 2003

RELATED-US-APPL-DATA:

child 10685435 A1 20031016

parent division-of 09566266 20000505 US PENDING

child 09566266 20000505 US

parent continuation-of PCT/EP98/07105 19981106 US UNKNOWN

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
EP	97870179.5	1997EP-97870179.5	November 6, 1997

US-CL-CURRENT: 435/5, 530/350 , 530/388.3

ABSTRACT:

Multimer peptides (e.g. 30- to 45-mer peptides) derived from hepatitis C virus envelope proteins reacting with the majority of anti-HCV antibodies present in patient sera are described. The usage of the latter peptides to diagnose, and to vaccinate against, an infection with hepatitis C virus is also disclosed.

---------- KWIC ---------

Detail Description Paragraph - DETX (18):

[0052] The term "functionally equivalent" as used in "functionally equivalent variant or fragment thereof" refers to variants and fragments of the peptides represented by SEQ ID 1 to 38, which bind anti-HCV-related virus antibodies. The term "variant or fragment" as used in "functionally equivalent variant or fragment thereof" refers to any variant or any fragment of the peptides represented by SEQ ID 1 to 38. Furthermore, the latter terms do not refer to, nor do they exclude, post-translational modifications of the peptides represented by SEQ ID 1 to 38 such as glycosylation, acetylation, phosphorylation, modifications with fatty acids and the like. Included within the definition are, for example, peptides containing one or more analogues of

an aa (including unnatural aa's), peptides with substituted linkages, mutated versions or natural sequence variations of the peptides (for examples corresponding to the genotypes HCV, as described in WO 94/12670 to Maertens et al.), peptides containing disulfide bounds between cysteine residues, or other cysteine modifications, biotinylated peptides, as well as other modifications known in the art. Modification of the structure of the polypeptides can be for such objectives as increasing therapeutic or prophylactic efficacy, stability (e.g. ex vivo shelf life and in vivo resistance to proteolytic degradation), or post-translational modifications (e.g. to alter the phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein are considered functional equivalents of the polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e. isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic: aspartate, glutamate; (2) basic: lysine, arginine, histidine; (3) nonpolar: alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar: glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic: aspartate, glutamate; (2) basic: lysin, arginine histidine, (3) aliphatic: glycine, alanine, valine, leucine, isoleucine, serine, threoaine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic: phenylalanine, tyrosine, tryptophan, (5) amide: asparagine, glutamine; and (6) sulfur-containing: cysteine and methionine. (see, for example, Biochemistry, 2nd ed., Ed. by L. Stryer, W H Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional homologue (e.g. functional in the sense that the resulting polypeptide mimics the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in e.g. ELISAs in a fashion similar to the wild-type protein, or to competitively inhibit such a response. Polypeptides in which more than one replacement has been introduced can be readily tested in the same manner. It should also be clear that the region of a peptide represented by SEQ ID 1 to 38 which bind to an antibody (the so-called epitope) need not to be composed of a contiguous aa sequence. In this regard, the term "fragment" includes any fragment which comprises these non-contiguous binding regions or parts thereof. In other words, fragments which include these binding regions may be separated by a linker, which is not a functional part of the epitope. This linker does not need to be an amino acid sequence, but can be any molecule, eg organic or inorganic, that allows the formation of the desired epitope by two or more fragments.

PGPUB-DOCUMENT-NUMBER: 20040121429

PGPUB-FILING-TYPE: corrected

DOCUMENT-IDENTIFIER: US 20040121429 A9

TITLE: Methods and compositions for modulating ACE-2 activity

PUBLICATION-DATE: June 24, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Parry, Tom J.	Walkersville	MD	US	
Sekut, Les	Ijamsville	MD	US	
Rosen, Craig A.	Laytonsville	MD	US	
Albert, Vivian R.	Rockville	MD	US	
Sanyal, Indrajit	Bethesda	MD	US	
Huang, Lili	Burlington	MA	US	
Wescott, Charles R.	Belmont	MA	US	

APPL-NO: 10/ 158825

DATE FILED: June 3, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60294976 20010604 US

US-CL-CURRENT: 435/69.1, 435/226 , 435/320.1 , 435/325 , 514/12 , 530/324

ABSTRACT:

Binding polypeptides comprising specific amino acid sequences are disclosed that specifically bind ACE-2 protein or ACE-2-like polypeptides. The binding polypeptides can be used in methods of the invention for detecting, isolating, or purifying ACE-2 protein or ACE-2-like polypeptides in solutions or mixtures, or biological samples. The invention also relates to nucleic acid molecules encoding these ACE-2 binding polypeptides, vectors and host cells containing these nucleic acids, and methods for producing the same. The present invention also relates to methods and compositions for detecting, diagnosing, prognosing, preventing, treating or ameliorating a disease or disorder associated with aberrant ACE-2 or ACE-2 receptor expression or inappropriate function of ACE-2 or ACE-2 receptor, comprising use of ACE-2 binding polypeptides or fragments or variants thereof, that specifically bind to ACE-2.

[0001] This application claims benefit under 35 U.S.C. .sctn.119(e) of U.S. Patent Application No. 60/294,976, filed Jun. 4, 2001, which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (10):

[0149] A "ACE-2 binding polypeptide" is a molecule of the invention that can bind an ACE-2 target protein. Non-limiting examples of ACE-2 binding polypeptides of the invention are the polypeptide molecules having an amino

acid sequence described herein (see SEQ ID NOs: 1-136). The term ACE-2 binding polypeptide also encompasses ACE-2 binding fragments and variants (including derivatives) of polypeptides having the specific amino acid sequences described herein (SEQ ID NOs: 1-136). By "variant" of an amino acid sequence as described herein is meant a polypeptide that binds ACE-2, but does not necessarily comprise an identical or similar amino acid sequence of an ACE-2 binding polypeptide specified herein. ACE-2 binding polypeptides of the invention which are variants of an ACE-2 binding polypeptide specified herein satisfy at least one of the following: (a) a polypeptide comprising, or alternatively consisting of, an amino acid sequence that is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, least 99%, or 100% identical to the amino acid sequence of an ACE-2 binding polypeptide sequence disclosed herein (SEQ ID NOs: 1-136), (b) a polypeptide encoded by a nucleotide sequence, the complementary sequence of which hybridizes under stringent conditions to a nucleotide sequence encoding an ACE-2 binding polypeptide disclosed herein (e.g., a nucleic acid sequence encoding the amino acid sequence of SEQ ID NOs: 1-136), and/or a fragment of an ACE-2 binding polypeptide disclosed herein, of at least 5 amino acid residues, at least 10 amino acid residues, at least 15 amino acid residues, or at least 20 amino acid residues. ACE-2 binding polypeptides of the invention also encompass polypeptide sequences that have been modified for various applications provided that such modifications do not eliminate the ability to bind an ACE-2 target. Specific, non-limiting examples of modifications contemplated include C-terminal or N-terminal amino acid substitutions or peptide chain elongations for the purpose of linking the ACE-2 bindor to a chromatographic material or other solid support. Other substitutions contemplated herein include substitution of one or both of a pair of cysteine residues that normally form disulfide links, for example with non-naturally occurring amino acid residues having reactive side chains, for the purpose of forming a more stable bond between those amino acid positions than the former disulfide bond. All such modified binding polypeptides are also considered ACE-2 binding polypeptides according to this invention so long as the modified polypeptides retain the ability to bind ACE-2 and/or ACE-2-like polypeptides, and therefore, may be used in one or more of the various methods described herein, such as, to detect, purify, or isolate ACE-2 or ACE-2-like polypeptides in or from a solution. ACE-2 binding polypeptides of the invention also include variants of the specific ACE-2 binding polypeptide sequences disclosed herein (e.g., SEQ ID NOs: 1-136) which have an amino acid sequence corresponding to one of these polypeptide sequences, but in which the polypeptide sequence is altered by substitutions, additions or deletions that provide for moleucles that bind ACE-2. Thus, the ACE-2 binding polypeptides include polypeptides containing, as a primary amino acid sequence, all or part of the particular ACE-2 binding polypeptide sequence including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence, resulting in a peptide which is functionally active. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Conservative substitutions for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Such ACE-2 binding polypeptides can be made either by chemical peptide synthesis or by recombinant production from a nucleic acid encoding the ACE-2 binding polypeptide which nucleic acid has been

mutated. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis, in vitro site-directed mutagenesis (Hutchinson et al., J. Biol. Chem., 253:6551 (1978)), use of TAB.RTM. linkers (Pharmacia), etc.

PGPUB-DOCUMENT-NUMBER: 20040102349

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040102349 A1

TITLE: Novel amylolytic enzyme extracted from bacillus sp.a 7-7 (dsm 12368) and washing and cleaning agents containing this novel amylolytic enzyme

PUBLICATION-DATE: May 27, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Breves, Roland	Ratingen		DE	
Maurer, Karl-Heinz	Erkrath		DE	
Kottwitz, Beatrix	Duesseldorf		DE	
Polanyi-Bald, Laura	Koeln		DE	
Hellebrandt, Angela	Koeln		DE	
Schmidt, Irmgard	Solingen		DE	
Stehr, Regina	Duesseldorf		DE	
Weber, Angrit	Bergisch-Gladbach		DE	

APPL-NO: 10/ 343212

DATE FILED: January 28, 2003

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
DE	100 36 752.6	2000DE-100 36 752.6	July 28, 2000
DE	100 36 753.4	2000DE-100 36 753.4	July 28, 2000

PCT-DATA:
APPL-NO: PCT/EP01/08359
DATE-FILED: Jul 19, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 510/392, 510/530

ABSTRACT:

The invention relates to a novel amylolytic enzyme extracted from the micro-organism Bacillus sp. A 7-7 (DSM 12368), to sufficiently similar proteins having an amylolytic function, to methods for the production thereof and to diverse fields of application for these proteins. In addition, they can be further developed beyond the implemented fields of application for other, above all, technical purposes. The invention particularly relates to washing and cleaning agents containing amylolytic proteins of the aforementioned type, to methods for cleaning textiles or hard surfaces that involve the use of such amylolytic proteins or analogous agents, and to their use for cleaning textiles or hard surfaces.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (66):

[0066] Of the variants falling within the similarity range mentioned above, those which have optimized properties for the potential applications envisaged are particularly preferred. As explained at the beginning, such variants can be produced by methods, preferably molecular-biological methods, known per se. For example, it would also be possible to delete methionine, tryptophane, cysteine and/or tyrosine residues of proteins according to the invention and/or to replace them with less readily oxidizable amino acid residues in accordance with the teaching of WO 94/18314. Oxidation stability, the pH activity profile and/or thermal stability can be improved in this way. Further developments through point mutagenesis may also be carried, for example, in accordance with WO 99/09183 and WO 99/23211.

PGPUB-DOCUMENT-NUMBER: 20040077013

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040077013 A1

TITLE: Protein secretion

PUBLICATION-DATE: April 22, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ashkenazi, Avi J.	San Mateo	CA	US	
Berman, Phillip W.	Portola Valley	CA	US	
Brousseau, David	San Francisco	CA	US	
Etcheverry, Tina	Berkeley	CA	US	

APPL-NO: 10/ 686887

DATE FILED: October 15, 2003

RELATED-US-APPL-DATA:

child 10686887 A1 20031015

parent continuation-of 09291925 19990414 US GRANTED

parent-patent 6693181 US

non-provisional-of-provisional 60082002 19980416 US

non-provisional-of-provisional 60123522 19990308 US

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/69.1 , 530/395 , 536/23.5

ABSTRACT:

DNA constructs, host cells and production methods are disclosed for the expression and recovery of polypeptides, especially those altered to have one or more glycosylation sites added or deleted. The DNA constructs, host cells and methods provided herein employ a DNA segment corresponding to a mammalian tissue plasminogen activator signal and/or pro peptide.

---------- KWIC ---------

Brief Description of Drawings Paragraph - DRTX (5):

[0019] FIGS. 4A-4C. Immunoprecipitation of TNFR-IgG1 glycosylation mutants. Plasmids encoding either TNFR-IgG1 or TNFR-IgG glycosylation site mutants were transfected into 293 cells using calcium phosphate precipitated DNA. Two days post-transfection the culture, medium was removed and replaced (after washing two times) with methionine- and cysteine-free DMEM supplemented with (.sup.35S)-labeled methionine and cysteine. Cells were labeled overnight at 37.degree. C. (5% CO.sub.2). Cell lysates and cell culture supernatants were precipitated by the addition of Protein A SEPHAROSE.TM.. The Protein A:TNFR-IgG1 complexes were pelleted by centrifugation, washed repeatedly and eluted in SDS-PAGE sample buffer containing mercaptoethanol. The eluted

protein was resolved on 10% SDS-PAGE gels and visualized by autoradiography. The glycosylation site mutants were examined in four separate experiments (FIGS. 4A-4D) where transiently expressed TNFR-IgG1 (TNFR-IgG 1) expressed in 293 cells or a stable CHO cell line expressing TNFR-IgG (TRY+) were used as positive controls. Background binding was determined in experiments with cells transfected with thrombopoeitin (TPO-). The mobilities of molecular weight markers are indicated at the left margins.

US-PAT-NO: 6869770

DOCUMENT-IDENTIFIER: US 6869770 B1

TITLE: Compositions and methods for early pregnancy diagnosis

DATE-ISSUED: March 22, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Roberts; Robert Michael	Columbia	MO	N/A	N/A
Green; Jonathan Andrew	Columbia	MO	N/A	N/A
Xie; Sancai	West Chester	OH	N/A	N/A

APPL-NO: 09/ 273164

DATE FILED: March 19, 1999

PARENT-CASE:

This application claims priority to U.S. Provisional Application Serial No. 60/078,783 filed Mar. 20, 1998 and U.S. Provisional Application Serial No. 60/106,188 filed Oct. 28, 1998. The entire text of each of the above-referenced disclosures is specifically incorporated by reference herein without disclaimer. The government may own rights in the present invention pursuant to grant R37 HD29483 and USDA grant 9601842.

US-CL-CURRENT: 435/7.1, 435/7.21 , 435/7.4 , 435/7.92 , 435/7.95 , 435/973 , 436/161 , 436/164 , 436/514 , 436/528 , 436/530 , 436/531

ABSTRACT:

Pregnancy-associated glycoproteins (PAGs) are structurally related to the pepsins, thought to be restricted to the hoofed (ungulate) mammals and characterized by being expressed specifically in the outer epithelial cell layer (chorion/trophectoderm) of the placenta. By cloning expressed genes from ovine and bovine placental cDNA libraries, the inventors estimate that cattle, sheep, and most probably all ruminant Artiodactyla, possess possibly 100 or more PAG genes, many of which are placentally expressed. The PAGs are highly diverse in sequence, with regions of hypervariability confined largely to surface-exposed loops. Selected PAG that are products of the iOnvasive binucleate cells, expressed highly in early pregnancy at the time of trophoblast invasion and expressed weakly, if at all, in late gestation are useful in the early diagnosis of pregnancy. In a preferred embodiment, the invention relates to immunoassays for detecting these PAGs.

24 Claims, 12 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 12

---------- KWIC ---------

Detailed Description Text - DETX (32):
It is contemplated that, for various uses, variants of PAGs can be utilized

according to the present invention. These changes may improve stability or function, for example, antigenicity or immunoreactivity. It may be desirable to create substitutional, insertional or deletion variants or fusion proteins from the identified PAGs. Deletion variants lack one or more residues of the native protein. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. This may include the insertion of an immunoreactive epitope or simply a single residue. Terminal additions, are fusion proteins. Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, such as stability against proteolytic cleavage, without the loss of other functions or properties. Substitutions of this kind may be termed "conservative," that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

US-PAT-NO: 6867012

DOCUMENT-IDENTIFIER: US 6867012 B2

TITLE: Determination method of biological component and reagent kit used therefor

DATE-ISSUED: March 15, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kishimoto; Takahide	Tsuruga	N/A	N/A	JP
Sogabe; Atsushi	Tsuruga	N/A	N/A	JP
Hattori; Shizuo	Tsuruga	N/A	N/A	JP
Oka; Masanori	Tsuruga	N/A	N/A	JP
Kawamura; Yoshihisa	Tsuruga	N/A	N/A	JP

APPL-NO: 09/ 998130

DATE FILED: December 3, 2001

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
JP	2000-370445	December 5, 2000
JP	2001-096724	March 29, 2001

US-CL-CURRENT: 435/15, 435/25 , 435/26 , 435/28 , 435/975

ABSTRACT:

The present invention provides novel glutathione-dependent formaldehyde dehydrogenase that makes possible quantitative measurement of formaldehyde by cycling reaction, and a determination method of formaldehyde and biological components, such as creatinine, creatine, and homocysteine, which produces formaldehyde as a reaction intermediate. In addition, the present invention provides a reagent kit for the above-mentioned determination method. The present invention provides a novel determination method of a homocysteine using transferase utilizing homocysteine and other compound as a pair of substrates. Particularly, the present invention provides a determination method of homocysteine which includes bringing betaine-homocysteine methyltransferase and dimethylglycine oxidase into contact with a sample and measuring produced hydrogen peroxide or formaldehyde. Moreover, the present invention provides novel dimethylglycine oxidase stable to thiol compound, which is suitably used for the measurement. The present invention provides a reagent kit used for any of the above-mentioned determination methods of homocysteine.

73 Claims, 4 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 2

---------- KWIC ---------

Brief Summary Text - BSTX (18):

Accordingly, the present invention provides the following. (1) A method for

determining formaldehyde, which comprises bringing glutathione-dependent formaldehyde dehydrogenase having a ratio of reactivity with thio-NAD to reactivity with NAD of not less than 30%, glutathione and an oxidized coenzyme into contact with a sample, and analyzing a compound resulting from the enzymatic reaction. (2) The method of the above-mentioned (1), wherein the ratio of reactivity with thio-NAD to reactivity with NAD of glutathione-dependent formaldehyde dehydrogenase is not less than 60%. (3) The method of the above-mentioned (1) or (2), wherein the glutathione-dependent formaldehyde dehydrogenase has the following physico-chemical properties: action: production of S-formylglutathione and reduced coenzyme by action on formaldehyde in the presence of one oxidized coenzyme selected from the group consisting of NADs, NADPs, thio-NADs and thio-NADPs and reduced glutathione optimal pH: about 7.5-about 8.5 pH stability: about 6.0-about 9.0, and heat stability: about 40.degree. C. or less (pH 7.5, 30 min). (4) The method of any of the above-mentioned (1) to (3), wherein the glutathione-dependent formaldehyde dehydrogenase is derived from microorganism. (5) The method of the above-mentioned (4), wherein the glutathione-dependent formaldehyde dehydrogenase is derived from methylotrophic yeast. (6) The method of the above-mentioned (5), wherein the glutathione-dependent formaldehyde dehydrogenase is derived from Hansenula yeast. (7) The method of the above-mentioned (6), wherein the glutathione-dependent formaldehyde dehydrogenase is derived from Hansenula nonfermentans IFO1473. (8) A method for determining formaldehyde, which comprises bringing glutathione-dependent formaldehyde dehydrogenase having a ratio of reactivity with thio-NAD to reactivity with NAD of not less than 30%, glutathione, one compound selected from the group consisting of thio-NADs and thio-NADPs, and one compound selected from the group consisting of reduced NADs and reduced NADPs into contact with a sample to allow cycling reaction and analyzing changes in the amount of a compound due to the reaction. (9) A method for determining formaldehyde, which comprises bringing glutathione-dependent formaldehyde dehydrogenase having a ratio of reactivity with thio-NAD to reactivity with NAD of not less than 30%, glutathione, one compound selected from the group consisting of reduced thio-NADs and reduced thio-NADPs, and one compound selected from the group consisting of NADs and NADPs into contact with a sample to allow cycling reaction and analyzing changes in the amount of a compound due to the reaction. (10) The method of the above-mentioned (8), wherein the amount of the reduced thio-NADP or reduced thio-NAD compound is analyzed. (11) The method of any of the above-mentioned (1)-(10), wherein a minimum detection limit of the formaldehyde is not more than 1 .mu.mol/L. (12) A method for determining a biological component, which comprises, in the determination of a biological component that produces formaldehyde as a reaction intermediate, measuring produced formaldehyde by the method of any of the above-mentioned (1)-(11). (13) A method for determining homocysteine, which comprises bringing betaine, betaine-homocysteine methyltransferase, dimethylglycine oxidase and, where necessary, sarcosine oxidase into contact with a sample, and measuring, according to the method of any of the above-mentioned (1)-(11), formaldehyde produced by the enzymatic reactions. (14) A method for determining creatine or creatinine, which comprises reacting creatine amidinohydrolase, sarcosine oxidase, and, where necessary, creatinine amidohydrolase and measuring, according to the method of any of the above-mentioned (1)-(11), formaldehyde produced by the enzymatic reactions. (15) A method for determining homocysteine, which comprises bringing transferase utilizing homocysteine and other compound as a pair of substrates and said other compound into contact with a sample and measuring the resulting compound. (16) The method of the above-mentioned (15), wherein the transferase and said other compound is a combination selected from the group consisting of betaine-homocysteine methyltransferase and betaine, betaine-homocysteine methyltransferase and dimethylthetin, homocysteine methyltransferase and S-adenosylmethionine, and N5-methyltetrahydrofolate-homocysteine methyltransferase and

N5-methyltetrahydrofolate, and the resulting compound is methionine. (17) The method of the above-mentioned (15), wherein the betaine, betaine-homocysteine methyltransferase, dimethylglycine oxidase and, where necessary, sarcosine oxidase are brought into contact with a sample, hydrogen peroxide produced by the enzymatic reactions is reacted with hydrogen donor chromogenic reagent and, where necessary, coupler, in the presence of peroxidase, and the resulting pigment is measured. (18) The method of the above-mentioned (15), wherein the betaine, betaine-homocysteine methyltransferase, dimethylglycine oxidase and, where necessary, sarcosine oxidase are brought into contact with a sample, formaldehyde produced by the enzymatic reactions is reacted with formaldehyde dehydrogenase and oxidized coenzyme and the resulting reduced coenzyme is measured. (19) The method of the above-mentioned (15), wherein the betaine, betaine-homocysteine methyltransferase, dimethylglycine oxidase and, where necessary, sarcosine oxidase are brought into contact with a sample, formaldehyde produced by the enzymatic reactions is reacted with glutathione, glutathione-dependent formaldehyde dehydrogenase and oxidized coenzyme and the resulting reduced coenzyme is measured. (20) The method of any of the above-mentioned (17)-(19), wherein the dimethylglycine oxidase is an enzyme stable to thiol compound. (21) The method of the above-mentioned (20), wherein the thiol compound is at least one kind selected from the group consisting of dithiothreitol, dithioerythritol, 2-mercaptoethanol, 2-mercaptoethanesulfonate, 2-mercaptoethylamine, cysteine, homocysteine, N-acetylcysteine, thioglycerol, thioglycolic acid, reduced glutathione and salts thereof. (22) The method of the above-mentioned (21), wherein the thiol compound is dithiothreitol. (23) The method of any of the above-mentioned (20)-(22), wherein the dimethylglycine oxidase shows an enzyme activity retained at least by 50% in the presence of 0.05 mmol/L dithiothreitol relative to the enzyme activity in the absence of dithiothreitol. (24) The method of any of the above-mentioned (20)-(23), wherein the dimethylglycine oxidase is an enzyme having the following physico-chemical properties: action: acting on dimethylglycine in the presence of oxygen to produce sarcosine, formaldehyde and hydrogen peroxide, and Km value for dimethylglycine: not more than 15 mM. (25) The method of any of the above-mentioned (20)-(24), wherein the dimethylglycine oxidase is derived from a microorganism. (26) The method of the above-mentioned (25), wherein the dimethylglycine oxidase is derived from a microorganism belonging to the genus Arthrobacter or the genus Streptomyces. (27) The method of the above-mentioned (26), wherein the dimethylglycine oxidase is derived from Arthrobacter nicotianae IFO14234 or Streptomyces mutabilis IFO12800. (28) The method of any of the above-mentioned (20)-(27), wherein a minimum detection limit of the homocysteine is not more than 1 .mu.mol/L. (29) Glutathione-dependent formaldehyde dehydrogenase having the following physico-chemical properties: action: acting on formaldehyde in the presence of one coenzyme selected from the group consisting of NADs, NADPs, thio-NADs and thio-NADPs, reduced glutathione to produce S-formylglutathione, a reduced coenzyme, a ratio of reactivity with thio-NAD to reactivity with NAD: not less than 30%, optimal pH: about 7.5-about 8.5, pH stability: about 6.0-about 9.0, and heat stability: about 40.degree. C. or less (pH 7.5, 30 min) (30) The glutathione-dependent formaldehyde dehydrogenase of the above-mentioned (29), which is derived from a microorganism. (31) The glutathione-dependent formaldehyde dehydrogenase of the above-mentioned (30), which is derived from methylotrophic yeast. (32) The glutathione-dependent formaldehyde dehydrogenase of the above-mentioned (31), which is derived from Hansenula yeast. (33) The glutathione-dependent formaldehyde dehydrogenase of the above-mentioned (32), which is derived from Hansenula nonfermentans IFO1473. (34) Dimethylglycine oxidase having the following physico-chemical properties:

US-PAT-NO: 6855318

DOCUMENT-IDENTIFIER: US 6855318 B1

TITLE: Multi-mer peptides derived from hepatitis C virus envelope proteins for diagnostic use and vaccination purposes

DATE-ISSUED: February 15, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Maertens; Geert	Brugge	N/A	N/A	BE
Depla; Erik	Dealalbergen	N/A	N/A	BE

APPL-NO: 09/ 566266

DATE FILED: May 5, 2000

PARENT-CASE:

This is a continuation of PCT application PCT/EP98/07105, filed 6 Nov. 1998, the entire content of which is hereby incorporated by reference in this application.

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
EP	97870179	November 6, 1997

US-CL-CURRENT: 424/189.1, 424/228.1 , 435/5 , 435/69.1 , 435/69.3 , 435/7.1 , 435/7.92 , 514/2

ABSTRACT:

Multimer peptides (e.g. 30- to 45-mer peptides) derived from hepatitis C virus envelope proteins reacting with the majority of anti-HCV antibodies present in patient sera are described. The usage of the latter peptides to diagnose, and to vaccinate against, an infection with hepatitis C virus is also disclosed.

29 Claims, 4 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 4

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Detailed Description Text - DETX (18):

The term "functionally equivalent" as used in "functionally equivalent variant or fragment thereof" refers to variants and fragments of the peptides represented by SEQ ID 1 to 38, which bind anti-HCV-related virus antibodies. The term "variant or fragment" as used in "functionally equivalent variant or fragment thereof" refers to any variant or any fragment of the peptides represented by SEQ ID 1 to 38. Furthermore, the latter terms do not refer to, nor do they exclude, post-translational modifications of the peptides

represented by SEQ ID 1 to 38 such as glycosylation, acetylation, phosphorylation, modifications with fatty acids and the like. Included within the definition are, for example, peptides containing one or more analogues of an aa (including unnatural aa's), peptides with substituted linkages, mutated versions or natural sequence variations of the peptides (for example corresponding to the genotypes HCV, as described in WO 94/12670 to Maertens et al.), peptides containing disulfide bounds between cysteine residues, or other cysteine modifications, biotinylated peptides, as well as other modifications known in the art. Modification of the structure of the polypeptides can be for such objectives as increasing therapeutic or prophylactic efficacy, stability (e.g. ex vivo shelf life and in vivo resistance to proteolytic degradation), or post-translational modifications (e.g. to alter the phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein are considered functional equivalents of the polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e. isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic: aspartate, glutamate; (2) basic: lysine, arginine, histidine; (3) nonpolar: alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar: glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic: aspartate, glutamate; (2) basic: lysin, arginine histidine, (3) aliphatic: glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic: phenylalanine, tyrosine, tryptophan; (5) amide: asparagine, glutamine; and (6) sulfur-containing: cysteine and methionine (see, for example, Biochemistry, 2nd ed., Ed. by L. Stryer, W H Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional homologue (e.g. functional in the sense that the resulting polypeptide mimics the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in e.g. ELISAs in a fashion similar to the wild-type protein, or to competitively inhibit such a response. Polypeptides in which more than one replacement has been introduced can be readily tested in the same manner.

US-PAT-NO: 6849450

DOCUMENT-IDENTIFIER: US 6849450 B2

TITLE: Antibodies to the metalloproteinase inhibitor

DATE-ISSUED: February 1, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Langley; Keith E.	Newbury Park	CA	N/A	N/A
DeClerck; Yves A.	Los Angeles	CA	N/A	N/A
Boone; Thomas C.	Newbury Park	CA	N/A	N/A

APPL-NO: 08/ 803954

DATE FILED: February 21, 1997

PARENT-CASE:

This application is a divisional of U.S. patent application Ser. No. 08/803,954, filed Feb. 21, 1997, which is a divisional of U.S. patent application Ser. No. 08/212,660, filed Mar. 11, 1994, now U.S. Pat. No. 5,714,465, which is a continuation of U.S. patent application Ser. No. 08/087,021, filed Jul. 6, 1993 now abandoned, which is a continuation of U.S. patent application Ser. No.07/710,728, filed Jun. 3, 1991, now abandoned, which is a continuation-in-part of U.S. patent application Ser. No. 07/501,904, filed Mar. 29, 1990, now abandoned, which is a continuation-in-part of U.S. patent application Ser. No. 07/355,027, filed May 19, 1989, pending, all of which are incorporated by reference herein.

US-CL-CURRENT: 435/331, 530/388.26 , 530/391.3

ABSTRACT:

A novel metalloproteinase inhibitor, analogs thereof, polynucleotides encoding the same, and methods of production, are disclosed. Pharmaceutical compositions and methods of treating disorders caused by excessive amounts of metalloproteinase are also disclosed.

4 Claims, 51 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 32

---------- KWIC --------

Detailed Description Text - DETX (260):

Deletion mutation is used to confirm the functional role of the N-terminal portion of MI and site-directed mutagenesis is used to investigate the role of specific cysteine residues in maintaining the stability and the activity of the molecule. cDNAs with deletions corresponding to the C-terminal end of MI were prepared using controlled exonucleotic cleavage of MI cDNA by exonuclease III. Alternatively, a cDNA with deletion of codons for amino acids 135 to 194 was obtained from the NcoI-StuI human MI cDNA using a unique NIa III restriction

site [C ATG.dwnarw. located at codon -26 (Methionine) and codon 135 (Methionine). A linker with a termination codon was then inserted and these constructs were reinserted into a pcDNA vector by blunt end ligation. This vector is suitable for expression in rat embryo cells and CHO cells. The vector was transfected into CHO cells and tested for transient expression. Alternatively, a pcD vector containing a SV40 promoter, splicing and polyadenylation sequences suitable for expression in COS cells is used [Okayama and Berg, Mol. Cell. Biol. 3,280-289 (1983)]. If needed, stable expression is obtained by co-transfection with plasmid pY3 containing the hygromycin B phosphotransferase gene [Blocklinger and Diegelman, Mol. Cell. Biol. 4,2929-2931 (1984)] and transfected cells are selected for resistance to hygromycin B (0.4 mg/ml) (see Example 12).

US-PAT-NO: 6830907

DOCUMENT-IDENTIFIER: US 6830907 B2

TITLE: Mutants of Mycobacterium vaccae-derived formate dehydrogenase and uses thereof

DATE-ISSUED: December 14, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Mitsuhashi; Kazuya	Niigata	N/A	N/A	JP
Yamamoto; Hiroaki	Ibaraki	N/A	N/A	JP
Kimoto; Norihiro	Ibaraki	N/A	N/A	JP

APPL-NO: 09/ 996008

DATE FILED: November 28, 2001

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
JP	2000-363894	November 29, 2000
JP	2001-254631	August 24, 2001

US-CL-CURRENT: 435/190, 435/132 , 435/189 , 435/252.3 , 435/440 , 435/90 , 536/23.2

ABSTRACT:

An objective of the present invention is to provide polypeptides capable of retaining a strong enzyme activity of formate dehydrogenase in the presence of an organic solvent and to provide the uses thereof.

Formate dehydrogenase mutant polypeptides, which are resistant to organic solvents, were constructed by substituting cysteines at position 146 and/or at position 256 in the amino acid sequence of Mycobacterium vaccae-derived formate dehydrogenase by site-directed mutagenesis. The polypeptides have strong activities of formate dehydrogenase in the presence of an organic solvent. The mutants are useful for the production of alcohols using ketones as raw material, etc.

66 Claims, 2 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 2

---------- KWIC ---------

Brief Summary Text - BSTX (8):

Tishkov et al. have shown that mutants of formate dehydrogenase from Pseudomonas sp. 101, in which the cysteine at position 256 has been substituted with serine or methionine by site-directed mutagenesis, have enhanced stability to mercury but reduced thermal stability (Biochem. Biophys. Res. Commun. 192:4480-4485, 1993). They have also reported mutants showing enhanced thermal stability, which were similarly created by substituting serine

with alanine, valine, or leucine at position 131, 160, 168, 184, or 228 (FEBS Letters 445:183-188, 1999).

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  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 17:13:00 ON 24 MAR 2005

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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

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       ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 17:13:15 ON 24 MAR 2005
ALL COPYRIGHTS AND RESTRICTIONS APPLY.  SEE HELP USAGETERMS FOR DETAILS.

11 FILES IN THE FILE LIST

=> s methionine and cysteine and muta?
FILE 'MEDLINE'
         43845 METHIONINE
         60923 CYSTEINE
        472784 MUTA?
L1         582 METHIONINE AND CYSTEINE AND MUTA?

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        455004 MUTA?
L2         381 METHIONINE AND CYSTEINE AND MUTA?

FILE 'LIFESCI'
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        209089 MUTA?
L3         195 METHIONINE AND CYSTEINE AND MUTA?

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L4         124 METHIONINE AND CYSTEINE AND MUTA?

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L5         492 METHIONINE AND CYSTEINE AND MUTA?

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L6         527 METHIONINE AND CYSTEINE AND MUTA?

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           863 OXIDAT?(3A)STAB?
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L14          3 L2 AND OXIDAT?(3A)STAB?

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L15          1 L3 AND OXIDAT?(3A)STAB?

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L18          1 L6 AND OXIDAT?(3A)STAB?

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                 (SULFUR(W)FREE)

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FILE 'SCISEARCH'
L38          0 L2 AND L26

FILE 'LIFESCI'
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FILE 'BIOTECHDS'
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FILE 'BIOSIS'
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FILE 'EMBASE'
L42          0 L6 AND L30

FILE 'HCAPLUS'
L43          2 L7 AND L31

FILE 'NTIS'
L44          0 L8 AND L32
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FILE 'BIOTECHNO'
L46             0 L10 AND L34

FILE 'WPIDS'
L47             0 L11 AND L35

TOTAL FOR ALL FILES
L48             2 L12 AND L36

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           863 OXIDAT?(3A)STAB?
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        971964 OXIDAT?
                 (OXIDAT? OR OXIDN)
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            624 OXIDAT?(3A)STAB?
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         108410 STAB?
            262 OXIDAT?(3A)STAB?
L58          35 MUTA? AND OXIDAT?(3A)STAB?

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          62048 OXIDN
             89 OXIDNS
         167188 OXIDAT?
                  (OXIDAT? OR OXIDN OR OXIDNS)
         762957 STAB?
           6628 OXIDAT?(3A)STAB?
L59          49 MUTA? AND OXIDAT?(3A)STAB?

TOTAL FOR ALL FILES
L60         625 MUTA? AND OXIDAT?(3A) STAB?

=> s l36(5a)(protein# or enzyme#)
FILE 'MEDLINE'
        1750768 PROTEIN#
         727138 ENZYME#
L61          10 L25(5A)(PROTEIN# OR ENZYME#)

FILE 'SCISEARCH'
        1391206 PROTEIN#
         457578 ENZYME#
L62           6 L26(5A)(PROTEIN# OR ENZYME#)

FILE 'LIFESCI'
         519500 PROTEIN#
         197115 ENZYME#
L63           4 L27(5A)(PROTEIN# OR ENZYME#)

FILE 'BIOTECHDS'
         135879 PROTEIN#
         122036 ENZYME#
L64           0 L28(5A)(PROTEIN# OR ENZYME#)

FILE 'BIOSIS'
        1664341 PROTEIN#
         769932 ENZYME#
L65           8 L29(5A)(PROTEIN# OR ENZYME#)

FILE 'EMBASE'
```

```
       1404525 PROTEIN#
        784597 ENZYME#
L66          5 L30(5A)(PROTEIN# OR ENZYME#)

FILE 'HCAPLUS'
       2003357 PROTEIN#
        925875 ENZYME#
L67         11 L31(5A)(PROTEIN# OR ENZYME#)

FILE 'NTIS'
         18014 PROTEIN#
         12029 ENZYME#
L68          0 L32(5A)(PROTEIN# OR ENZYME#)

FILE 'ESBIOBASE'
        648995 PROTEIN#
        224372 ENZYME#
L69          2 L33(5A)(PROTEIN# OR ENZYME#)

FILE 'BIOTECHNO'
        653195 PROTEIN#
        353854 ENZYME#
L70          2 L34(5A)(PROTEIN# OR ENZYME#)

FILE 'WPIDS'
        141070 PROTEIN#
         78510 ENZYME#
L71          1 L35(5A)(PROTEIN# OR ENZYME#)

TOTAL FOR ALL FILES
L72         49 L36(5A)(PROTEIN# OR ENZYME#)

=> s l36 and oxidat?(3a)stab?
FILE 'MEDLINE'
        191608 OXIDAT?
        375646 STAB?
           863 OXIDAT?(3A)STAB?
L73          0 L25 AND OXIDAT?(3A)STAB?

FILE 'SCISEARCH'
        344417 OXIDAT?
        720082 STAB?
          4392 OXIDAT?(3A)STAB?
L74          0 L26 AND OXIDAT?(3A)STAB?

FILE 'LIFESCI'
         37669 OXIDAT?
        111731 STAB?
           212 OXIDAT?(3A)STAB?
L75          0 L27 AND OXIDAT?(3A)STAB?

FILE 'BIOTECHDS'
          9317 OXIDAT?
         36044 STAB?
           132 OXIDAT?(3A)STAB?
L76          0 L28 AND OXIDAT?(3A)STAB?

FILE 'BIOSIS'
        200635 OXIDAT?
        403546 STAB?
          2077 OXIDAT?(3A)STAB?
L77          0 L29 AND OXIDAT?(3A)STAB?

FILE 'EMBASE'
```

```
        165775 OXIDAT?
        354558 STAB?
           803 OXIDAT?(3A)STAB?
L78          0 L30 AND OXIDAT?(3A)STAB?

FILE 'HCAPLUS'
        576167 OXIDAT?
        708326 OXIDN
        971964 OXIDAT?
                 (OXIDAT? OR OXIDN)
       1450757 STAB?
         17679 OXIDAT?(3A)STAB?
L79          3 L31 AND OXIDAT?(3A)STAB?

FILE 'NTIS'
         25520 OXIDAT?
        107522 STAB?
           624 OXIDAT?(3A)STAB?
L80          1 L32 AND OXIDAT?(3A)STAB?

FILE 'ESBIOBASE'
         69706 OXIDAT?
        159101 STAB?
           565 OXIDAT?(3A)STAB?
L81          0 L33 AND OXIDAT?(3A)STAB?

FILE 'BIOTECHNO'
         43160 OXIDAT?
        108410 STAB?
           262 OXIDAT?(3A)STAB?
L82          0 L34 AND OXIDAT?(3A)STAB?

FILE 'WPIDS'
        138733 OXIDAT?
         62048 OXIDN
            89 OXIDNS
        167188 OXIDAT?
                 (OXIDAT? OR OXIDN OR OXIDNS)
        762957 STAB?
          6628 OXIDAT?(3A)STAB?
L83          4 L35 AND OXIDAT?(3A)STAB?

TOTAL FOR ALL FILES
L84          8 L36 AND OXIDAT?(3A) STAB?

=> s (124 or 148 or 160 or 172 or 184) not 2001-2005/py
FILE 'MEDLINE'
       2327968 2001-2005/PY
L85         40 (L13 OR L37 OR L49 OR L61 OR L73) NOT 2001-2005/PY

FILE 'SCISEARCH'
       4315369 2001-2005/PY
L86         48 (L14 OR L38 OR L50 OR L62 OR L74) NOT 2001-2005/PY

FILE 'LIFESCI'
        413541 2001-2005/PY
L87         23 (L15 OR L39 OR L51 OR L63 OR L75) NOT 2001-2005/PY

FILE 'BIOTECHDS'
         95279 2001-2005/PY
L88         37 (L16 OR L40 OR L52 OR L64 OR L76) NOT 2001-2005/PY

FILE 'BIOSIS'
       2116147 2001-2005/PY
```

```
L89          45 (L17 OR L41 OR L53 OR L65 OR L77) NOT 2001-2005/PY

FILE 'EMBASE'
       2005140 2001-2005/PY
L90          34 (L18 OR L42 OR L54 OR L66 OR L78) NOT 2001-2005/PY

FILE 'HCAPLUS'
       4390500 2001-2005/PY
L91          77 (L19 OR L43 OR L55 OR L67 OR L79) NOT 2001-2005/PY

FILE 'NTIS'
         61001 2001-2005/PY
L92           1 (L20 OR L44 OR L56 OR L68 OR L80) NOT 2001-2005/PY

FILE 'ESBIOBASE'
       1217536 2001-2005/PY
L93          21 (L21 OR L45 OR L57 OR L69 OR L81) NOT 2001-2005/PY

FILE 'BIOTECHNO'
        368875 2001-2005/PY
L94          25 (L22 OR L46 OR L58 OR L70 OR L82) NOT 2001-2005/PY

FILE 'WPIDS'
       3982123 2001-2005/PY
L95          16 (L23 OR L47 OR L59 OR L71 OR L83) NOT 2001-2005/PY

TOTAL FOR ALL FILES
L96         367 (L24 OR L48 OR L60 OR L72 OR L84) NOT 2001-2005/PY

=> fil .becpat
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    21.53      21.74

FILES 'BIOTECHDS, HCAPLUS, WPIDS' ENTERED AT 17:19:46 ON 24 MAR 2005
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3 FILES IN THE FILE LIST

=> s (l24 or l48 or l60 or l72 or l84) and wo/pc and pry<=2000 range=2004,
FILE 'BIOTECHDS'
           8033 WO/PC
            886 PRY<=2000
                  (PRY<=2000)
L97           0 (L16 OR L40 OR L52 OR L64 OR L76) AND WO/PC AND PRY<=2000

FILE 'HCAPLUS'
          66948 WO/PC
          67381 PRY<=2000
L98           0 (L19 OR L43 OR L55 OR L67 OR L79) AND WO/PC AND PRY<=2000

FILE 'WPIDS'
         143533 WO/PC
          55799 PRY<=2000
                  (PRY<=2000)
L99           0 (L23 OR L47 OR L59 OR L71 OR L83) AND WO/PC AND PRY<=2000

TOTAL FOR ALL FILES
L100          0 (L24 OR L48 OR L60 OR L72 OR L84) AND WO/PC AND PRY<=2000

=> log y
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     7.97      29.71
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STN INTERNATIONAL LOGOFF AT 17:20:41 ON 24 MAR 2005